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OM protein - protein search, using sw model

Run on: June 27, 2003, 17:15:16 ; Search time 14.3 Seconds
(without alignments)
73.950 Million cell updates/sec

Title: US-10-019-439-1
Perfect score: 57
Sequence: 1 GPRVERHOSA 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	644	1 FGHUA	fibrinogen alpha c
2	57	100.0	644	2 D44224	fibrinogen alpha c
3	47	82.5	628	2 A05296	fibrinogen alpha c
4	46	80.7	311	2 A05294	fibrinogen alpha c
5	38	66.7	299	1 S60035	senescence marker
6	38	66.7	550	1 FGRFA	fibrinogen alpha c
7	37	64.9	336	2 S65566	inward rectifier p
8	36	63.2	108	2 T34436	hypothetical prote
9	36	63.2	552	2 F96769	hypothetical prote
10	36	63.2	581	1 RYEC2	DNA primase (EC 2.
11	36	63.2	581	2 D85967	DNA biosynthesis,
12	36	63.2	581	2 E91122	DNA primase (limpor
13	35	61.4	65	2 S36971	hypothetical prote
14	35	61.4	299	2 S72173	senescence marker
15	35	61.4	299	2 S34588	senescence marker
16	35	61.4	428	2 H72304	histidinol dehydro
17	35	61.4	639	2 T06735	hypothetical prote
18	34.5	60.5	121	2 AF2798	hypothetical prote
19	34	59.6	67	2 G89853	hydrogenase-relate
20	34	59.6	161	2 G43255	myb-related transc
21	34	59.6	218	2 T51681	synthetaxin 8 relat
22	34	59.6	292	2 T49339	antimethyltransfe
23	34	59.6	346	2 B90243	heparin cofactor I
24	34	59.6	399	2 B83030	probable propionyl
25	34	59.6	499	2 A37924	hypothetical prote
26	34	59.6	529	2 D70719	alpha-glucosidase
27	34	59.6	558	2 S75927	alpha-glucosidase
28	34	59.6	584	1 ALBY	alpha-glucosidase
29	34	59.6	584	2 S46183	alpha-glucosidase

30	34	59.6	584	2 S64627	alpha-glucosidase
31	34	59.6	950	2 B87611	tonB-dependent rec
32	34	59.6	1004	2 S51133	transposase Tn4652
33	34	59.6	1539	2 T30037	hypothetical prote
34	34	59.6	3472	2 T31308	hypothetical 367X
35	33	57.9	209	2 AC0273	probable exported
36	33	57.9	263	2 AH0644	probable exported
37	33	57.9	331	2 B82341	NifH3/Sm1 family
38	33	57.9	352	1 AJKXO	glutamate-ammonia
39	33	57.9	456	2 B75434	UDP-N-acetylglucos
40	33	57.9	478	2 E86314	F2H15.15 protein -
41	33	57.9	533	2 H86282	protein F10B6.34 l
42	33	57.9	587	2 D84426	hypothetical prote
43	33	57.9	589	2 S50355	alpha-glucosidase
44	33	57.9	589	2 S59370	alpha-glucosidase
45	33	57.9	589	2 S66856	probable membrane

ALIGNMENTS

RESULT 1

FGHUA
Fibrinogen alpha chain precursor, short splice form [validated] - human
N/Alternate names: coagulation factor I
N/Contains: fibrinopeptide A
C/Species: Homo sapiens (man)
C/Date: 24-Apr-1984 #sequence revision 30-Jun-1987 #text change 08-Dec-2000
A/Accession: A93956; A43568; A90468; I84456; A44234; C44234; B94433; A90433; B94309; S1
R/Kant, J.A.; Lord, S.T.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 80, 3953-3957, 1983
A/Title: Partial mRNA sequences for human Alpha, Beta, and gamma fibrinogen chains: e
A/Reference number: A93956; MUID:83247396; PMID:6575389
A/Accession: A93956
A/Molecule type: mRNA
A/Residues: 1-644 <KAN>
A/Cross-references: GB:000128; NID:g182425; PIDN:AA52427.1; PID:g182426
A/Note: The authors translated the codon GAG for residue 247 as Gly, GGA for residue 43
R/Chung, D.W.; Harris, J.E.; Davie, E.W.
Adv. Exp. Med. Biol. 281, 39-48, 1990
A/Title: Nucleotide sequences of the three genes coding for human fibrinogen.
A/Reference number: A43568; MUID:91344740; PMID:2102623
A/Accession: A43568
A/Molecule type: DNA
A/Residues: 1-330 'A', 332-644 <CHU>
A/Cross-references: GB:M64982; NID:g458553; PIDN:AA17055.1; PID:g458554
R/Rixon, M.W.; Chan, W.Y.; Davie, E.W.; Chung, D.W.
Biochemistry 22, 3237-3244, 1983
A/Title: Characterization of a complementary deoxyribonucleic acid coding for the alpha
A/Reference number: A90468; MUID:83283432; PMID:6688355
A/Accession: A90468
A/Molecule type: mRNA
A/Residues: 1-330 'A', 332-629 <RIX>
A/Cross-references: GB:000127; NID:g182423; PIDN:AA52426.1; PID:g182424
R/Imam, A.M.A.; Eaton, M.A.W.; Williamson, R.; Humphries, S.
Nucleic Acids Res. 11, 7427-7434, 1983
A/Title: Isolation and characterization of cDNA clones for the Alpha- and gamma-chains
A/Reference number: I37393; MUID:84069777; PMID:6689067
A/Accession: I84456
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 110-156 <RES>
A/Cross-references: GB:K02272; NID:g182427; PIDN:AA52428.1; PID:g182428
R/Ry, Y.; Weissbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redm
Biochemistry 31, 11968-11972, 1992
A/Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a nov
A/Reference number: A44234; MUID:93090725; PMID:1457396
A/Accession: A44234
A/Molecule type: mRNA
A/Residues: 1-51 <PUT>
A/Cross-references: GB:M64982; NID:g458553; PIDN:AA17055.1; PID:g458554
A/Note: Sequence extracted from NCBI backbone (NCBIN:119912, NCBIN:119914, NCBIP:119918
A/Accession: C44234

A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 605-644 <F02>
 A/Cross-references: GB:M64982, NID:9458553, PIDN:AAA17055.1; PID:9458554
 A/Note: Sequence extracted from NCBI backbone (NCBI:119920)
 R/Henschel, A.; Lottspeich, F.; Souhan, C.; Topfer-Petersen, E.
 in Proteins of the Biological Fluids, Proc. 28th Colloq., Peeters, H., ed., pp.51-56, Pe
 A/Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural v
 A/Reference number: A94433
 A/Accession: B94433
 A/Molecule type: protein
 A/Residues: 20-214, 'RS', 217-298, 'G', 300-303, 'G', 305-629 <HEN>
 R/Watt, K.W.K.; Cottrell, B.A.; Strong, D.D.; Doolittle, R.F.
 Biochemistry 18, 5410-5416, 1979
 A/Title: Amino acid sequence studies on the alpha chain of human fibrinogen. Overlappin
 A/Reference number: A90433; MUID:80088231; PMID:518846
 A/Contents: disulfide bonds
 A/Accession: A90433
 A/Molecule type: protein
 A/Residues: 20-146, 'Q', 148-195, 'N', 197-230, 'N', 232-316, 'SG', 319-406, 'D', 408, 'N', 410-629
 R/Blomback, B.; Hessel, B.; Hoger, D.
 Thromb. Res. 8, 639-658, 1976
 A/Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
 A/Reference number: A94309; MUID:7625080; PMID:936108
 A/Contents: variant, and disulfide bonds
 A/Accession: B94309
 A/Molecule type: protein
 A/Residues: 20-65, 'T', 67-629 <BLO>
 R/Dewey, R.S.; Llesch, J.M.; Williams, H.R.; Sugg, E.E.; Dolan, C.A.; Davies, P.; Mumfor
 Biochem. J. 281, 519-524, 1992
 A/Title: Purification and characterization by fast-atom-bombardment mass spectrometry of
 incubation with calcium ionophore A23187.
 A/Reference number: S19297; MUID:92143822; PMID:1136899
 A/Accession: S19297
 A/Molecule type: protein
 A/Residues: 20-40 <DEM>
 R/Retzius, A.D.; Markland Jr., F.S.
 Thromb. Res. 52, 541-552, 1988
 A/Title: A direct-acting fibrinolytic enzyme from the venom of Agkistrodon contortrix co
 A/Reference number: A60905; MUID:89162316; PMID:3232124
 A/Accession: A60905
 A/Molecule type: protein
 A/Residues: 433-451 <RET>
 R/Fretto, L.J.; Ferguson, E.W.; Steinman, H.M.; McKee, P.A.
 J. Biol. Chem. 253, 2184-2195, 1978
 A/Title: Localization of the alpha-chain cross-link acceptor sites of human fibrin.
 A/Reference number: A92225; MUID:78130085; PMID:632262
 A/Contents: annotation; cross-linking acceptor sites
 R/Cottrell, B.A.; Strong, D.D.; Watt, K.W.K.; Doolittle, R.F.
 Biochemistry 18, 5405-5410, 1979
 A/Title: Amino acid sequence studies on the alpha chain of human fibrinogen. Exact locat
 A/Reference number: A90433; MUID:80088230; PMID:518845
 A/Contents: annotation; cross-linking acceptor sites
 R/Henschel, A.; Lottspeich, F.; Kehl, M.; Souhan, C.
 Ann. N. Y. Acad. Sci. 408, 28-43, 1983
 A/Title: Covalent structure of fibrinogen.
 A/Reference number: A90037; MUID:83254370; PMID:6575689
 A/Contents: annotation; review, disulfide bonds
 R/Liarte, E.; Plana, M.; Guasch, M.D.; Martos, C.
 Biochem. Biophys. Res. Commun. 117, 631-636, 1983
 A/Title: Phosphorylation of fibrinogen by casein kinase 1.
 A/Reference number: A90116; MUID:84104274; PMID:6318767
 A/Contents: annotation; phosphorylation
 A/Note: About one-third of alpha chain molecules in blood were found to be phosphorylate
 R/Doolittle, R.F.
 Annu. Rev. Biochem. 53, 195-229, 1984
 A/Title: Fibrinogen and fibrin
 A/Reference number: A90041; MUID:84305751; PMID:6383194
 A/Contents: annotation; review, EM structure, polymerization, ligands
 R/Kimura, S.; Aoki, N.
 J. Biol. Chem. 261, 15591-15595, 1986
 A/Title: Cross-linking site in fibrinogen for alpha-2-plasmin inhibitor.
 A/Reference number: A92565; MUID:87057130; PMID:2877981

A/Contents: annotation; cross-linking site for alpha-2-plasmin inhibitor
 R/Kristnamurthi, S.; Dickens, T.A.; Patel, Y.; Wheeler-Jones, C.P.D.; Kakkar, V.V.
 Biochem. Biophys. Res. Commun. 163, 1256-1264, 1989
 A/Title: The fibrinogen-derived peptide (RGDS) prevents proteolytic degradation of pro
 A/Reference number: A33261; MUID:89392031; PMID:2783116
 A/Contents: annotation; activity of cell attachment (R-G-D) motif
 R/Kirschbaum, N.E.; Budzynski, A.Z.
 J. Biol. Chem. 265, 13669-13676, 1990
 A/Title: A unique proteolytic fragment of human fibrinogen containing the Alpha COOH-t
 A/Reference number: A71171; MUID:90337977; PMID:2143188
 A/Contents: annotation; hemectin cleavage site
 A/Note: hemectin, a protease from Haemaphysa ghilianii, the giant South American leech
 R/Staendker, L.; Sillard, R.; Bench, K.W.; Ruff, A.; Rada, M.; Schulz-Knappe, P.; Sche
 Biochem. Biophys. Res. Commun. 215, 996-902, 1995
 A/Title: In vivo degradation of human fibrinogen A alpha: Detection of cleavage sites a
 A/Reference number: J04334; MUID:96027996; PMID:7488058
 A/Contents: annotation; composition and amino-terminal sequences of carboxyl end peptid
 C/Comment: Unlike the beta and gamma chains, the alpha chain is not glycosylated.
 C/Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibronectin.
 C/Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleav
 iation sites responsible for the formation of the soft clot.
 C/Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabil
 izer) and between alpha chains (weaker) of different monomers.
 C/Comment: All fibrinogen chains are synthesized in the liver.
 C/Comment: See PIR:D44234 for the minor alternative splice form.
 C/Genetics:
 A/Gene: GDB:FGA
 A/Cross-references: GDB:119129; OMIM:134820
 A/Map position: 4q28-4q28
 A/Intons: 18/3; 60/3; 122/1; 171/2
 A/Note: The list of introns is incomplete
 C/Complex: The fibrinogen molecule is a hexamer containing two sets of alpha, beta (see
 ins are contained in the core. Two three-chain coiled coils emerge from this core and c
 C/Function:
 A/Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
 A/Pathway: blood coagulation
 C/Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
 C/Keywords: alternative splicing; blood coagulation; coiled coil, glycoprotein; liver;
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-35/Product: fibrinogen alpha chain #status experimental <MAT>
 F:36-629/Product: fibrin alpha chain #status experimental <APT>
 F:36-629/Region: polymerization site, binding to the distal domain of the gamma chain of
 F:57-185/Domain: fibrinogen disulfide ring homology <PDR>
 F:57-593/Region: cell attachment (R-G-D) motif
 F:52,460/Binding site: phosphate (Ser) (covalent) #status experimental
 F:35-36/Cleavage site: Arg-Gly (thrombin) #status experimental
 F:47/Disulfide bonds: interchain (to alpha-47) #status experimental
 F:55/Disulfide bonds: interchain (to beta-95) #status experimental
 F:54/Disulfide bonds: interchain (to gamma-49) #status experimental
 F:68/Disulfide bonds: interchain (to beta-106) #status experimental
 F:184/Disulfide bonds: interchain (to gamma-165) #status experimental
 F:184/Disulfide bonds: interchain (to beta-223) #status experimental
 F:288,419/Binding site: carboxylate (Asn) (covalent) #status absent
 F:322/Cross-link: isopeptide (Lys) (interchain to Gln-41 of alpha-2-plasmin inhibitor)
 F:347,385/Cross-link: isopeptide (Gln) (interchain to Lys-N6-amino of alpha) #status ex
 F:461,491/Disulfide bonds: #status experimental
 F:527,558,575,581,599/Cross-link: isopeptide (Lys) (interchain to Gln of alpha) #status ex
 Query Match 100.0%; Score 57; DB 1; Length 644;
 Best Local Similarity 100.0%; Pred. No. 0.0048;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRVVERHQA 11
 DB 36 GPRVVERHQA 46
 RESULT 2
 D44234
 fibrinogen alpha chain precursor, extended splice form - human
 N/Alternate names: coagulation factor I

N/Contains: fibrinopeptide A
 C/Species: Homo sapiens (man)
 C/Date: 10-Jun-1993 #sequence_revision 06-Sep-1996 #text_change 19-Jan-2001
 C/Accession: D44234; B44234
 R/Fu, Y.; Weisbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redm
 Biochemistry 31, 11968-11972, 1992
 A/Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a nove
 A/Reference number: A44234; MUID:93090725; PMID:1457396
 A/Accession: D44234
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA; DNA
 A/Residues: 1-866 <FU1>
 A/Cross-references: GB:M58569; NID:g182406; PID:g182407
 A/Note: neither the complete nucleic acid sequence nor the complete translation are show
 A/Accession: B44234
 A/Molecule type: mRNA; DNA
 A/Residues: 605-866 <FU2>
 A/Note: sequence extracted from NCBI backbone (NCBIP:119917)
 C/Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibrinectin.
 C/Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleave
 ization sites responsible for the formation of the soft clot.
 C/Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabiliz
 ger) and between alpha chains (weaker) of different monomers.
 C/Comment: All fibrinogen chains are synthesized in the liver.
 C/Comment: See PIR:FEHUA for the major splice form. It is not known whether this form is
 C/Genetics:
 A/Gene: GDB:FGA
 A/Cross-references: GDB:119129; OMIM:134820
 A/Map position: 4q28-4q28
 A/Intons: 18/3; 60/3; 122/1; 171/2
 A/Note: the list of introns is incomplete
 C/Complex: The fibrinogen molecule is a hexamer containing two sets of three nonidentical
 ntained in the core. Two three-chain coiled coils emerge from this core and connect it to
 distal domain nodes.
 C/Function:
 A/Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
 A/Pathway: blood coagulation
 C/Superfamily: human extended splice form fibrinogen alpha chain; fibrinogen beta/gamma
 C/Keywords: alternative splicing; blood coagulation; glycoprotein; liver; phosphoprotein
 F/1-19/Domin: signal sequence #status predicted <SIG>
 F/20-863/Product: fibrinogen alpha chain, extended splice form #status predicted <MAT>
 F/20-35/Product: fibrinopeptide A #status experimental <APT>
 F/35-863/Product: fibrin alpha chain, extended splice form #status predicted <FGA>
 F/57-185/Domin: fibrinogen disulfide ring homology <FDR>
 F/591-593/Region: cell attachment (R-G-D) motif
 F/629-663/Domin: fibrinogen beta/gamma homology <FBG>
 F/22,460/Binding site: phosphate (Ser) (covalent) #status experimental
 F/35-36/Cleavage site: Arg-Gly (thrombin) #status experimental
 F/47/Dsulfide bonds: interchain (to alpha-47) #status experimental
 F/55/Dsulfide bonds: interchain (to beta-95) #status experimental
 F/64/Dsulfide bonds: interchain (to gamma-49) #status experimental
 F/66/Dsulfide bonds: interchain (to beta-106) #status experimental
 F/180/Dsulfide bonds: interchain (to gamma-165) #status experimental
 F/184/Dsulfide bonds: interchain (to beta-223) #status experimental
 F/288,419/Binding site: carboxylate (Asn) (covalent) #status absent
 F/332/Cross-link: isopeptide (Lys) (interchain to Gln-41 of alpha-2-plasmin inhibitor) #
 F/347,385/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of alpha) #status exp
 F/461-491/Dsulfide bonds: #status experimental
 F/527,558,575,581,599/Cross-link: isopeptide (Lys) (interchain to Gln of alpha) #status
 F/66,831/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 57; DB 2; Length 866;
 Best Local Similarity 100.0%; Pred. No. 0 0065;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPRVERHQA 11
 |||||
 Db 36 GPRVERHQA 46

RESULT 3
 A05296
 Fibrinogen alpha chain - dog (fragment)

C/Species: Canis lupus familiaris (dog)
 C/Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 25-Oct-1996
 C/Accession: A94308; A03118; A37511; A05296; B37511; C03118
 R/Birken, S.; Wilner, G.D.; Canfield, R.E.
 Thromb. Res. 7, 599-610, 1975
 A/Title: Studies of the structure of canine fibrinogen.
 A/Reference number: A94308; MUID:76081726; PMID:1198547
 A/Accession: A94308
 A/Molecule type: protein
 A/Residues: 1-28 <BIR>
 R/Blomback, B.; Blomback, M.; Groendahl, N.J.
 Acta Chem. Scand. 19, 1789-1791, 1965
 A/Title: Studies on fibrinopeptides from mammals.
 A/Reference number: A03118
 A/Accession: A03118
 A/Molecule type: protein
 A/Residues: 1-16 <BUO>
 R/Osbahr Jr., A.D.; Colman, R.W.; Laki, K.; Gladner, J.A.
 Biochem. Biophys. Res. Commun. 14, 555-558, 1964
 A/Reference number: A37511; MUID:66020594; PMID:5836555
 A/Accession: A37511
 A/Molecule type: protein
 A/Residues: 1, 'D', 3, 'EGKO', 8-16 <OSB>
 C/Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
 C/Keywords: blood coagulation; liver; phosphoprotein; plasma
 F/1-16/Product: fibrinopeptide A #status experimental <APT>
 F/3/Binding site: phosphate (Ser) (covalent) (partial) #status experimental

Query Match 82.5%; Score 47; DB 2; Length 28;
 Best Local Similarity 81.8%; Pred. No. 0.018;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GPRVERHQA 11
 |||||
 Db 17 GPRVERHQA 27

RESULT 4
 A05294
 Fibrinogen alpha chain - bovine (fragments)
 N/Contains: fibrinopeptide A
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 05-Jun-1987 #sequence_revision 10-Mar-1994 #text_change 31-Mar-2000
 C/Accession: A05294; A25715; A03117; A37505; A37506; B37505; C03117
 R/Henschen, A.; Lottspeich, F.; Topfer-Petersen, E.; Kehl, M.; Timpl, R.
 in Proceedings of the Biological Fluids, Proc. 28th Colloq., ed. Peeters, H., pp. 47-50, Pe
 A/Reference number: A05294
 A/Accession: A05294
 A/Molecule type: protein
 A/Residues: 20-26, 'Y', 28-49:55-80:81-108 <HEN>
 R/Chung, D.W.; Rixon, M.W.; Davie, E.W.
 in Proteins in Biology and Medicine, Bradshaw, R.A., ed., pp. 309-328, Academic Press, N
 A/Title: The biosynthesis of fibrinogen and the cloning of its cDNA.
 A/Reference number: A25715
 A/Accession: A25715
 A/Molecule type: mRNA
 A/Residues: 109-311 <CHU>
 R/Sjogquist, J.; Blomback, B.; Wallen, P.
 Ark. Kemi 16, 425-436, 1960
 A/Title: Amino acid sequence of bovine fibrinopeptides.
 A/Reference number: A03117
 A/Accession: A03117
 A/Molecule type: protein
 A/Residues: 1-19 <SUO>
 R/Folk, J.E.; Gladner, J.A.; Levin, Y.
 J. Biol. Chem. 234, 2317-2320, 1959
 A/Title: Thrombin-induced formation of co-fibrin. III. Acid degradation studies and sum
 A/Reference number: A37505
 A/Accession: A37505
 A/Molecule type: protein
 A/Residues: 1-19 <FOL>
 R/Timpl, R.; Fietzek, P.P.; Wachter, E.; van Delden, V.
 Biochim. Biophys. Acta 490, 420-429, 1977

A>Title: Disulfide-linked cyanogen bromide peptides of bovine fibrinogen. II. Isolation
 A/Reference number: A37506; MUID:77112616; PMID:836881
 A/Accession: A37506
 A/Molecule type: protein
 A/Residues: 20-54 <TIM>
 R/Martinielli, R.A.; Ingalls, A.S.; Rubira, M.R.; Hageman, T.C.; Hurrell, J.G.R.; Leach, S
 Arch. Biochem. Biophys. 192, 27-32, 1979
 A>Title: Amino acid sequences of portions of the alpha and beta chains of bovine fibrin
 A/Reference number: A37507; MUID:79164394; PMID:434821
 A/Accession: A37507
 A/Molecule type: protein
 A/Residues: 23-52 <MAR>
 C/Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
 C/Keywords: blood coagulation; liver; plasma
 F.1-19/Product: fibrinopeptide A #status experimental <APT>
 F.20-31/Product: fibrinogen alpha chain (fragments) #status experimental <MAT>

Query Match 80.7%; Score 46; DB 2; Length 311;
 Best Local Similarity 81.8%; Pred. No. 0.32;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GPRVERHOSA 11
 |||:|||||
 Db 20 GPRIVERQOSA 30

RESULT 5
 S60035
 senescence marker protein 30 - human
 N/Alternate names: regucalcin
 C/Species: Homo sapiens (man)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
 C/Accession: S60035; 152491
 R/Fujita, T.; Mandel, J.L.; Shirasawa, T.; Hino, O.; Shirai, T.; Matuyama, N.
 Biochim. Biophys. Acta 1263, 249-252, 1995
 A>Title: Isolation of cDNA clone encoding human homologue of senescence marker protein-3
 A/Reference number: 152491; MUID:96004897; PMID:7548213
 A/Accession: S60035
 A/Molecule type: mRNA
 A/Residues: 1-299 <FUJ>
 A/Cross-references: EMBL:DJ1815; NID:g1072311; PIDN:BA06602.1; PID:g1072312
 C/Genetics:
 A:Gene: GDB:RCN; RC; SMP30
 A/Cross-references: GDB:9955055
 A/Map position: Xp11.3-Xp11.2
 C/Superfamily: senescence marker protein-30
 C/Keywords: calcium binding

Query Match 66.7%; Score 38; DB 1; Length 299;
 Best Local Similarity 70.0%; Pred. No. 11;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRVERHOSA 11
 |||:|||||
 Db 124 PAVDERHOGA 133

RESULT 6
 FGRTA
 fibrinogen alpha chain precursor - rat
 N/Contains: fibrinopeptide A
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 25-Oct-1996
 C/Accession: A92915; B03118; A03119
 R/Cabriere, G.R.; Comeau, C.M.; Fowlkes, D.M.; Fornace Jr., A.J.; Malley, J.D.; Kant, J.
 J. Mol. Biol. 185, 1-19, 1985
 A>Title: Evolution and structure of the fibrinogen genes. Random insertion of introns on
 A/Reference number: A92915; MUID:86011580; PMID:4046033
 A/Accession: A92915
 A/Molecule type: DNA
 A/Residues: 1-550 <CRA>
 R:Blombaeck, B.; Blombaeck, M.; Groendahl, N.J.
 Acta Chem. Scand. 19, 1789-1791, 1965

A>Title: Studies on fibrinopeptides from mammals.
 A/Reference number: A03118
 A/Accession: B03118
 A/Molecule type: protein
 A/Residues: 20-29 <BLO>
 C/Comment: Unlike the beta and gamma chains, the alpha chain is not glycosylated.
 C/Comment: Fibrinogen chains are synthesized in the liver.
 C/Genetics:
 A/Introns: 18/3; 61/3; 123/1; 171/3
 C/Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
 C/Keywords: blood coagulation; liver; plasma; platelet
 F.1-19/Domin: signal sequence #status predicted <SIG>
 F.20-36/Product: fibrinopeptide A #status experimental <APT>
 F.37-55/Product: fibrinogen alpha chain #status predicted <MPT>
 F.56-166/Domin: fibrinogen disulfide ring homology <PDR>
 F.48/Disulfide bonds: interchain (to alpha-48) #status predicted
 F.56/59,188/Disulfide bonds: interchain (to beta chain) #status predicted
 F.65/Disulfide bonds: interchain (to gamma-49) #status predicted
 F.181/Disulfide bonds: interchain (to gamma-165) #status predicted
 F.404-434/Disulfide bonds: #status predicted

Query Match 66.7%; Score 38; DB 1; Length 550;
 Best Local Similarity 70.0%; Pred. No. 21;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GPRVERHOS 10
 |||:|||||
 Db 37 GPRIVEROPS 46

RESULT 7
 S65566
 inward rectifier potassium channel TWIK-1 - human
 C/Species: Homo sapiens (man)
 C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
 C/Accession: S65566
 R/Lesage, F.; Gullimare, E.; Fink, M.; Duprat, F.; Lazdunski, M.; Romey, G.; Barhanin,
 EMBO J. 15, 1004-1011, 1996
 A>Title: TWIK-1, a ubiquitous human weakly inward rectifying K(+) channel with a novel
 A/Reference number: S65566; MUID:96183184; PMID:8605869
 A/Accession: S65566
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-336 <LES>
 A/Cross-references: EMBL:U33632; NID:g1086490; PIDN:AA01688.1; PID:g1086491

Query Match 64.9%; Score 37; DB 2; Length 336;
 Best Local Similarity 77.8%; Pred. No. 20;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 RVERHOSA 11
 |||:|||||
 Db 12 RVERHOSA 20

RESULT 8
 T34436
 hypothetical protein K11H12.1 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
 C/Accession: T34436
 R/Bradshaw, H.
 submitted to the EMBL Data Library, February 1997
 A/Description: The sequence of C. elegans cosmid K11H12.
 A/Reference number: Z21526
 A/Accession: T34436
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-108 <BRA>
 A/Cross-references: EMBL:U88168; PIDN:AAC24398.1; GSPDB:GN00022; CESP:K11H12.1
 A/Experimental source: strain Bristol N2; clone K11H12
 C/Genetics:
 A:Gene: CESP:K11H12.1

A:Map position: 4
 A:Introns: 22/3; 61/3
 C:Superfamily: bola protein

Query Match 63.2%; Score 36; DB 2; Length 108;
 Best Local Similarity 66.7%; Pred. No. 9.9;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPRVERHQ 9
 |||||
 56 GKRYERHR 64

RESULT 9
 F96769
 hypochloral protein P9611.8 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: F96769
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Jensen, N.F.; Hughes, B.; Hutzar, L.
 Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marzalli, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: F96769
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-552 <STO>
 A:Cross-references: GB:AE05173; NID:G10092419; PIDN:AA12824.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F9611.8
 A:Map position: 1

Query Match 63.2%; Score 36; DB 2; Length 552;
 Best Local Similarity 63.6%; Pred. No. 52;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GPRVERHQA 11
 |||||
 121 GPRVERHQA 131

RESULT 10
 RYEC2
 DNA primase (EC 2.7.7.-) - Escherichia coli (strain K-12)
 C:Species: Escherichia coli
 C:Date: 20-Sep-1994 #sequence_revision 20-Sep-1994 #text_change 01-Mar-2002
 C:Accession: A03423; H65094; A03422; I77532
 R:Burton, Z.F.; Gross, C.A.; Matanabe, K.K.; Burgess, R.R.
 Cell 32, 335-349, 1983
 A:Title: The operon that encodes the sigma subunit of RNA polymerase also encodes ribosome
 A:Reference number: A02749; MUID:83129424; PMID:6186393
 A:Accession: A03423
 A:Molecule type: DNA
 A:Residues: 1-581 <BUR>
 A:Cross-references: GB:U01687; NID:G147753; PIDN:AAA24600.1; PID:G147755
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617; PMID:9278503
 A:Accession: H65094
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-581 <BLAT>
 A:Cross-references: GB:AE000389; GB:U00096; NID:G1789441; PIDN:AAC76102.1; PID:G1789447;
 A:Experimental source: strain K-12, substrain MG1655

R:Smiley, B.L.; Lupski, J.R.; Svec, P.S.; McMacken, R.; Godson, G.N.
 Proc. Natl. Acad. Sci. U.S.A. 79, 4550-4554, 1982
 A:Title: Sequences of the Escherichia coli dnaG primase gene and regulation of its expr
 A:Reference number: A03422; MUID:83014926; PMID:6750604
 A:Accession: A03422
 A:Molecule type: DNA
 A:Residues: 1-23, 'N', 25-105, 'XDRAPSEANALSDGSEYVLTFTTCCHVCAVSG', 145-156, 'GLVLR', 1
 R:Lupski, J.R.; Smiley, B.L.; Godson, G.N.
 Mol. Gen. Genet. 189, 48-57, 1983
 A:Title: Regulation of the rpsu-dnaG-rpoD macromolecular synthesis operon and the initi
 A:Reference number: I57721; MUID:83218520; PMID:6222240
 A:Accession: I77532
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-23, 'N', 25-81 <RES>
 A:Cross-references: EMBL:V00346; NID:G42867; PIDN:CAA23636.1; PID:G42869
 C:Comment: This enzyme, an RNA polymerase, interacts with DNA to synthesize the primer
 C:Genetics:
 A:Gene: dnaG
 A:Map position: 67 min
 C:Superfamily: DNA primase
 C:Keywords: DNA replication; nucleotidyltransferase

Query Match 63.2%; Score 36; DB 1; Length 581;
 Best Local Similarity 66.7%; Pred. No. 55;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPRVERHQ 9
 |||||
 104 GPRVERHQ 112

RESULT 11
 D85967
 DNA biosynthesis, DNA primase [imported] - Escherichia coli (strain O157:H7, substrain
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001
 C:Accession: D85967
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: D85967
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-581 <STO>
 A:Cross-references: GB:AE005174; NID:G12517648; PIDN:AAG58200.1; GSPDB:GN00145; UWGP:24
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: dnaG
 C:Superfamily: DNA primase

Query Match 63.2%; Score 36; DB 2; Length 581;
 Best Local Similarity 66.7%; Pred. No. 55;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPRVERHQ 9
 |||||
 104 GPRVERHQ 112

RESULT 12
 E91122
 DNA primase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
 C:Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 27-Nov-2001
 C:Accession: E91122
 R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurakawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
 gasawara, N.; Yasunaga, T.; Kihara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
 A:Reference number: A99629; MUID:21156231; PMID:11258796

A:Accession: E91122
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-581 <HAV>
 A:Cross-references: GB:BA000007; PIDN:BA837372.1; PID:913363422; GSPDB:GN00154
 A:Experimental source: strain O157:H7, substrain RIMD 0509952
 C:Genetics:
 A:Gene: ECS3949
 C:Superfamily: DNA primase

Query Match 63.2%; Score 36; DB 2; Length 581;
 Best Local Similarity 66.7%; Pred. No. 55;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GPRVERHQ 9
 Db 104 GPSQIERHQ 112

RESULT 13
 S36971
 Hypothetical protein 5 - *Synechococcus* sp. (PCC 6716)
 C:Species: *Synechococcus* sp.
 A:Variety: PCC 6716
 C:Date: 22-Jan-1994 #sequence_revision 12-Apr-1996 #text_change 08-Oct-1999
 C:Accession: S36971; S31895
 R:van Walraven, H.S.; Lutter, R.; Walker, J.E.
 Biochem. J. 294, 239-251, 1993
 A:Title: Organization and sequences of genes for the subunits of ATP synthase in the
 A:Reference number: S36960; MUID:93371369; PMID:8363578
 A:Accession: S36971
 A:Molecule type: DNA
 A:Residues: 1-65 <VAN>
 A:Cross-references: EMBL:X70431; NID:949213; PIDN:CAA49881.1; PID:949225
 A:Experimental source: PCC 6716

Query Match 61.4%; Score 35; DB 2; Length 65;
 Best Local Similarity 45.5%; Pred. No. 9.3;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GPRVERHQSA 11
 Db 17 GPRVYORHNS 27

RESULT 14
 S72173
 senescence marker protein 30 - mouse
 N:Alternate names: regucalcin
 C:Species: *Mus musculus* (house mouse)
 C:Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 20-Sep-1999
 C:Accession: S72173; S72174
 R:Fujita, T.; Shirasawa, T.; Maruyama, N.
 Biochim. Biophys. Acta 1308, 49-57, 1996
 A:Title: Isolation and characterization of genomic and cDNA clones encoding mouse senesc
 A:Reference number: S72173; MUID:96328264; PMID:8765750
 A:Accession: S72173
 A:Molecule type: mRNA
 A:Residues: 1-299 <FTU>
 A:Cross-references: EMBL:U28937; NID:91143999; PIDN:AAC52721.1; PID:91144000
 A:Accession: S72174
 A:Molecule type: DNA
 A:Residues: 1-54 <FWW>
 A:Cross-references: EMBL:U32170; NID:91144337; PIDN:AAD03478.1; PID:91144338
 A:Experimental source: liver
 C:Function:
 A:Description: calcium binding
 A:Note: age-associated decrease
 C:Superfamily: senescence marker protein-30
 C:Keywords: calcium binding

Query Match 61.4%; Score 35; DB 2; Length 299;
 Best Local Similarity 60.0%; Pred. No. 44;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PRVERHQSA 11
 Db 124 PAVLRHQGS 133

RESULT 15
 S34588
 senescence marker protein SMP-30 - rat
 N:Alternate names: regucalcin
 C:Species: *Rattus norvegicus* (Norway rat)
 C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
 C:Accession: S34588; S34589; S27203
 R:Shimokawa, N.; Yamaguchi, M.
 FEBS Lett. 327, 251-255, 1993
 A:Title: Molecular cloning and sequencing of the cDNA coding for a calcium-binding pro
 A:Reference number: S34588; MUID:93351639; PMID:8348951
 A:Accession: S34588
 A:Molecule type: mRNA
 A:Residues: 1-299 <SHI>
 A:Cross-references: GB:D38467; GB:D14327; GB:D16386; NID:9600378; PIDN:BA07490.1; PID
 A:Accession: S34589
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 84-299 <SH2>
 A:Cross-references: EMBL:D14327
 R:Fujita, T.; Shirasawa, T.; Uchida, K.; Maruyama, N.
 Biochim. Biophys. Acta 1132, 297-305, 1992
 A:Title: Isolation of cDNA clone encoding rat senescence marker protein-30 (SMP30) and
 A:Reference number: S27203; MUID:93041931; PMID:1420310
 A:Accession: S27203
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-147, 'D', '149-299 <FTU>
 A:Cross-references: EMBL:X69021; NID:957254; PIDN:CAA48786.1; PID:957255
 C:Superfamily: senescence marker protein-30
 C:Keywords: calcium binding

Query Match 61.4%; Score 35; DB 2; Length 299;
 Best Local Similarity 60.0%; Pred. No. 44;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PRVERHQSA 11
 Db 124 PAVLRHQGS 133

Search completed: June 27, 2003, 17:18:35
 Job time : 16.3 secs

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OM protein - protein search, using sw model

Run on: June 27, 2003, 17:13:51 ; Search time 7.7 Seconds
(without alignments)
59.252 Million cell updates/sec

Title: US-10-019-439-1
Perfect score: 57
Sequence: 1 GPRVERHOSA 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	866	FIBA_HUMAN	P02671 homo sapien
2	47	82.5	28	FIBA_CANFA	P02673 canis fami1
3	46	80.7	596	FIBA_BOVIN	P02672 bos taurus
4	38	66.7	299	SM30_HUMAN	Q15493 homo sapien
5	38	66.7	623	Y711_HUMAN	Q94819 homo sapien
6	38	66.7	782	FIBA_RAT	P03639 rattus norv
7	37	64.9	336	C1W1_HUMAN	O00180 homo sapien
8	37	64.9	336	C1W1_MOUSE	O08581 mus musculu
9	36	63.2	108	YNI1_CAEEL	P91375 caenorhabdi
10	36	63.2	581	PRIM_ECOLI	P02923 escherichia
11	35	61.4	299	SM30_MOUSE	O64374 mus musculu
12	35	61.4	299	SM30_RABIT	Q9U116 oryctolagus
13	35	61.4	299	SM30_RAT	Q03336 rattus norv
14	34	59.6	161	H0XO_ALCEU	P31910 alcaligenes
15	34	59.6	399	PNB1_PSEAE	Q9H944 pseudomonas
16	34	59.6	499	HEP2_HUMAN	P05546 homo sapien
17	34	59.6	558	MADE_SYNY3	P74292 synechocyst
18	34	59.6	584	MAIS_YEAST	P53341 saccharomyc
19	34	59.6	584	MAIS_YEAST	P53341 saccharomyc
20	34	59.6	584	MAIS_YEAST	P53341 saccharomyc
21	33	57.9	209	MA6S_YEAST	P07255 saccharomyc
22	33	57.9	352	GNL2_FRALP	Q82633 yersinia pe
23	33	57.9	432	YO31_MYCTU	P19300 mycobacteri
24	33	57.9	513	VL2_COPY	Q69892 canine oral
25	33	57.9	589	MAIS_YEAST	P40439 saccharomyc
26	33	57.9	589	MAIS_YEAST	P40439 saccharomyc
27	33	57.9	4451	GRSB_BACBR	P14668 b graximicid
28	32	56.1	29	GALA_AMICA	P47214 amia calva
29	32	56.1	117	GALA_CHICK	P30802 gallus gall
30	32	56.1	182	TER5_BP21	Q96669 bacterioph co
31	32	56.1	207	RNFG_HABIN	P44291 haemophilus
32	32	56.1	208	HAN2_BRARE	P57102 brachydanio
33	32	56.1	208	HAN2_BRARE	P57102 brachydanio

34	32	56.1	245	1	YG24_YEAST	P53237 saccharomyc
35	32	56.1	313	1	MRW_XYLF	Q9P188 xylella fas
36	32	56.1	327	1	CP27_PIG	P79402 sus scrofa
37	32	56.1	371	1	KLBI_ECOLI	P52604 escherichia
38	32	56.1	464	1	RCCL_CANAL	P52459 candida alb
39	32	56.1	489	1	CP26_CANFA	O62671 canis fami1
40	32	56.1	544	1	PYRG_ECOLI	P08398 escherichia
41	32	56.1	550	1	PHNL_DESGI	P12944 desulfovibr
42	32	56.1	590	1	VPP_BP2	P25479 bacterioph
43	32	56.1	700	1	MADE_SCHPO	O74940 schistosach
44	32	56.1	778	1	TAST_HUMAN	Q12815 homo sapien
45	32	56.1	968	1	BCAL_RAT	O63767 rattus norv

ALIGNMENTS

RESULT 1
FIBA_HUMAN STANDARD; PRT; 866 AA.
AC P02671; Q9BX62; Q9UCB2;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen alpha/alpha-E chain precursor [Contains: Fibrinopeptide A].
GN FGA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ALPHA-E FORM).
RX MEDLINE=93090725; PubMed=1457396;
RA Fu Y., Weissbach L., Plant P.W., Oddoux C., Cao Y., Liang T.J.,
RA Roy S.N., Redman C.W., Grieninger G.;
RT "Carboxy-terminal-extended variant of the human fibrinogen alpha
RT subunit: a novel exon conferring marked homology to beta and gamma
RT subunits.";
RL Biochemistry 31:11968-11972(1992).
RN [2]
RP SEQUENCE FROM N.A. (ALPHA-E FORM).
RA Chung D.W., Grieninger G.;
RT "Fibrinogen DNA and protein sequences.";
RL (in) Ebert R.F. (eds.);
RL Index of variant human fibrinogens, pp.13-24, CRC Press,
RL Boca Raton (1994).
RN [3]
RP SEQUENCE FROM N.A. (ALPHA-E; ALPHA), AND VARIANTS VAL-6; ALA-331 AND
RP ALA-456.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-655 FROM N.A. (ALPHA-E FORM).
RC TISSUE=Liver;
RX MEDLINE=91344740; PubMed=2102623;
RA Chung D.W., Harris J.E., Davie E.W.;
RT "Nucleotide sequences of the three genes coding for human
RT fibrinogen.";
RL Adv. Exp. Med. Biol. 281:39-48(1990).
RN [5]
RP SEQUENCE FROM N.A. (ALPHA FORM).
RX MEDLINE=83247396; PubMed=6575389;
RA Kant J.A., Lord S.T., Crabtree G.R.;
RT "Partial mRNA sequences for human A alpha, B beta, and gamma
RT fibrinogen chains: evolutionary and functional implications.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3953-3957(1983).
RN [6]
RP SEQUENCE OF 1-629 FROM N.A.
RX MEDLINE=83283432; PubMed=6688355;
RA Rixon M.W., Chan W.-Y., Davie E.W., Chung D.W.;
RT "Characterization of a complementary deoxyribonucleic acid coding for
RT the alpha chain of human fibrinogen.";

- RL Biochemistry 22:3237-3244(1983).
RN [7]
RP SEQUENCE OF 20-629.
RA Henschen A., Lotzspeich F., Southan C., Topfer-Petersen E.;
RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
RL structural variants."; (in) Peeters H. (eds.);
RN Provides of the biological fluids, Proc. 28th colloquium, pp.51-56,
RL Pergamon Press, Oxford (1980).
RP [8]
RP SEQUENCE OF 20-629, AND DISULFIDE BONDS.
RA MEDLINE=80086231; PubMed=518846;
RT Watt K.W.K., Cottrell B.A., Strong D.D., Doollittle R.F.;
RN "Amino acid sequence studies on the alpha chain of human fibrinogen.
RT Overlapping sequences providing the complete sequence.";
RL Biochemistry 18:5410-5416(1979).
RN [9]
RP SEQUENCE OF 110-156 FROM N.A.
RA MEDLINE=84069777; PubMed=6689067;
RT Itam A.M., Eaton M.A., Williamson R., Humphries S.;
RN "Isolation and characterization of cDNA clones for the A alpha- and
RT gamma-chains of human fibrinogen.";
RL Nucleic Acids Res. 11:7427-7434(1983).
RN [10]
RP SEQUENCE OF 605-644 FROM N.A. (ALPHA FORM).
RA MEDLINE=83254384; PubMed=6575700;
RT Chung D.W., Rixon M.W., Que B.G., Davie E.W.;
RN "Cloning of fibrinogen genes and their cDNA.";
RT Ann. N.Y. Acad. Sci. 408:449-456(1983).
RN [11]
RP SEQUENCE OF 20-35.
RA Blomback B., Blomback M., Gron Dahl N.J., Guthrie C., Hinton M.;
RT "Studies on fibrinopeptides from primates.";
RL Acta Chem. Scand. 19:1788-1789(1965).
RN [12]
RP CROSS-LINKING ACCEPTOR SITES.
RA MEDLINE=80088230; PubMed=518845;
RT Cottrell B.A., Strong D.D., Watt K.W.K., Doollittle R.F.;
RN "Amino acid sequence studies on the alpha chain of human fibrinogen.
RT Exact location of cross-linking acceptor sites.";
RL Biochemistry 18:5405-5410(1979).
RN [13]
RP CROSS-LINKING ACCEPTOR SITES.
RA MEDLINE=78130085; PubMed=632262;
RT Fretto L.J., Ferguson E.W., Steinman H.M., McKee P.A.;
RN "Localization of the alpha-chain cross-link acceptor sites of human
RT fibrin.";
RL J. Biol. Chem. 253:2184-2195(1978).
RN [14]
RP VARIANT AND DISULFIDE BONDS.
RA MEDLINE=76225080; PubMed=936108;
RT Blomback B., Hessel B., Hogg D.;
RN "Disulfide bridges in NH2-terminal part of human fibrinogen.";
RT Thromb. Res. 8:639-658(1976).
RN [15]
RP REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
RA MEDLINE=84305751; PubMed=6383194;
RT Doollittle R.F.;
RN "Fibrinogen and fibrin.";
RL Annu. Rev. Biochem. 53:195-229(1984).
RN [16]
RP CROSS-LINKING SITE FOR ALPHA-2-PLASMIN INHIBITOR.
RA MEDLINE=87057190; PubMed=2877981;
RT Kimura S., Aoki N.;
RN "Cross-linking site in fibrinogen for alpha 2-plasmin inhibitor.";
RT J. Biol. Chem. 261:15591-15595(1986).
RN [17]
RP PHOSPHORYLATION.
RA MEDLINE=84104274; PubMed=6318767;
RT Itarte E., Plana M., Guasch M.D., Martos C.;
RN "Phosphorylation of fibrinogen by casein kinase 1.";
RT Biochem. Biophys. Res. Commun. 117:631-636(1983).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 26-39.
RA MEDLINE=92218459; PubMed=1560020;
RT Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edwards B.F.P.;
RN "The structure of residues 7-16 of the A alpha-chain of human
RT fibrinogen bound to bovine thrombin at 2.3-A resolution.";
RL J. Biol. Chem. 267:7911-7920(1992).
RN [19]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 130-216.
RA MEDLINE=97472408; PubMed=933233;
RT Spraggon G., Everse S.J., Doollittle R.F.;
RN "Crystal structures of fragment D from human fibrinogen and its
RT crosslinked counterpart from fibrin.";
RL Nature 389:455-462(1997).
RN [20]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 130-216.
RA MEDLINE=98292395; PubMed=9628725;
RT Everse S.J., Spraggon G., Veerapandian L., Riley M., Doollittle R.F.;
RN "Crystal structure of fragment double-D from human fibrin with two
RT different bound ligands.";
RL Biochemistry 37:8637-8642(1998).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 670-866.
RA MEDLINE=98356117; PubMed=9689040;
RT Spraggon G., Applegate D., Everse S.J., Zhang J.Z., Veerapandian L.,
RN Reeman C., Doollittle R.F., Griening G.;
RT "Crystal structure of a recombinant alphaBEC domain from human
RL fibrinogen-420.";
RN Proc. Natl. Acad. Sci. U.S.A. 95:9099-9104(1998).
RN [22]
RP X-RAY CRYSTALLOGRAPHY.
RA MEDLINE=99175089; PubMed=10074346;
RT Everse S.J., Spraggon G., Veerapandian L., Doollittle R.F.;
RN "Conformational changes in fragments D and double-D from human
RT fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
RL Biochemistry 38:2941-2946(1999).
RN [23]
RP VARIANT KYOTO-2.
RA MEDLINE=91300048; PubMed=2070049;
RT Yoshida N., Okuma W., Hirata H., Matsuda M., Yamazumi K., Aekura S.;
RN "Fibrinogen Kyoto II, a new congenitally abnormal molecule,
RT characterized by the replacement of A alpha proline-18 by leucine.";
RL Blood 78:149-153(1991).
RN [24]
RP VARIANT LIMA.
RA MEDLINE=92240580; PubMed=1634621;
RT Maekawa H., Yamazumi K., Muramatsu S., Kaneko M., Hirata H.,
RN Takahashi N., Arocha-Pinango C.L., Rodriguez S., Nagy H.,
RA Perez-Requejo J.L., Matsuda M.;
RT "Fibrinogen Lima: a homozygous dysfibrinogen with an A
RN alpha-arginine-141 to serine substitution associated with extra
RT N-glycosylation at A alpha-asparagine-139. Impaired fibrin gel
RT formation but normal fibrin-tactilated plasminogen activation
RN catalyzed by tissue-type plasminogen activator.";
RL J. Clin. Invest. 90:67-76(1992).
RN [25]
RP VARIANT CARACAS-2.
RA MEDLINE=91268018; PubMed=1675636;
RT Maekawa H., Yamazumi K., Muramatsu S., Kaneko M., Hirata H.,
RN Takahashi N., de Bosch N.B., Carvajal Z., Ojeda A.,
RA Arocha-Pinango C.L., Matsuda M.;
RT "An A alpha Ser-434 to N-glycosylated Asn substitution in a
RN dysfibrinogen, fibrinogen Caracas II, characterized by impaired
RT fibrin gel formation.";
RL J. Biol. Chem. 266:11575-11581(1991).
RN [26]
RP VARIANT DUSART.
RA MEDLINE=92232289; PubMed=8473507;
RT Koopman J., Haverkate F., Grimbergen J., Lord S.T., Mosseson M.W.,
RN Diorio J.P., Stebenlist K.S., Legrand C., Soria J., Soria C.,
RA "Molecular basis for fibrinogen Dusart (A alpha 554 Arg->Cys) and
RT its association with abnormal fibrin polymerization and
RN thrombophilia.";

Query Match 100.0%; Score 57; DB 1; Length 866;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPRVERHOSA 11
 |||||
 Db 36 GPRVERHOSA 46

RESULT 2

FIBA_CANFA STANDARD; PRT; 28 AA.
 ID FIBA_CANFA
 AC P02673; P14464;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fibrinogen alpha chain [contains: Fibrinopeptide A] (Fragment).
 GN FGA.
 OS Canis familiaris (Dog), and
 OS Vulpes vulpes (Red fox).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615, 9627;
 RN (1)
 RP SEQUENCE.
 RC SPECIES=C.familiaris;
 RX MEDLINE=76081726; Pubmed=1198547;
 RA Birken S., Wilner G.D., Canfield R.E.;
 RT "Studies of the structure of canine fibrinogen."
 RL Thromb. Res. 7:599-610(1975).
 RN (2)
 RP SEQUENCE OF 1-16.
 RC SPECIES=C.familiaris, and V.vulpes;
 RA Blomback B., Blomback M., Grondahl N.J.;
 RT "Studies on fibrinopeptides from mammals."
 RL Acta Chem. Scand. 19:1789-1791(1965).
 RN (3)
 RP SEQUENCE OF 1-16.
 RC SPECIES=C.familiaris;
 RX MEDLINE=66020594; Pubmed=5836555;
 RA Obbahr A.J., Jr., Colman R.W., Laki K., Gladner J.A.;
 RT "The nature of the peptides released from canine fibrinogen."
 RL Biochem. Biophys. Res. Commun. 14:555-558(1964).
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.

DR PIR; A03118; A03118.
 DR PIR; A05296; A05296.
 KM Blood coagulation; Plasma; Phosphorylation.
 FT PEPTIDE 1 16 FIBRINOPEPTIDE A.
 FT MOD RES 2 3 PHOSPHORYLATION (IN SOME MOLECULES).
 FT CONFLICT 2 2 N -> D (IN REF. 2).
 FT NON TER 4 7 KEKE -> ESKQ (IN REF. 2).
 SQ SEQUENCE 28 AA; 2958 MW; 09DCD3F923BFEB2 CRC64;

Query Match 82.5%; Score 47; DB 1; Length 28;
 Best Local Similarity 81.8%; Pred. No. 0.0054;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPRVERHOSA 11
 |||||
 Db 17 GPRIVERXOSA 27

RESULT 3

FIBA_BOVIN STANDARD; PRT; 596 AA.
 ID FIBA_BOVIN
 AC P02672; O97642;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fibrinogen alpha chain [contains: Fibrinopeptide A] (Fragment).
 GN FGA.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE OF 155-558 FROM N.A.
 RA Murakawa M.;
 RT Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE OF 393-596 FROM N.A.
 RA Chung D.W., Rixon M.W., Davie E.W.;
 RT "The biosynthesis of fibrinogen and the cloning of its cDNA."
 RL (in) Bradshaw R.A. (eds.);
 RL Proteins in biology and medicine, pp.309-328, Academic Press,
 RL New York (1982).
 RN (3)
 RP SEQUENCE OF 1-19.
 RA Sjoquist J., Blomback B., Wallen P.;
 RT "Amino acid sequence of bovine fibrinopeptides."
 RL Ark. Kent 16:425-436(1960).
 RN (4)
 RP SEQUENCE OF 1-19.
 RA Polk J.E., Gladner J.A., Levin Y.;
 RT "Thrombin-induced formation of co-fibrin. III. Acid degradation
 RT studies and summary of sequential evidence on peptide A."
 RL J. Biol. Chem. 234:2317-2320(1959).
 RN (5)
 RP SEQUENCE OF 20-54.
 RX MEDLINE=77112616; Pubmed=836881;
 RA Timpl R., Fietzek P.P., Wachter E., van Delden V.;
 RT "Disulfide-linked cyanogen bromide peptides of bovine fibrinogen. II.
 RT Isolation and sequence analysis of the chain constituents from the
 RT amino terminal region."
 RL Biochim. Biophys. Acta 490:420-429(1977).
 RN (6)
 RP SEQUENCE OF 23-52.
 RX MEDLINE=79164394; Pubmed=434821;
 RA Martinelli R.A., Inglis A.S., Rubira M.R., Hageman T.C.,
 RA Hurteal J.G.R., Leach S.J., Scheraga H.A.;
 RT "Amino acid sequences of portions of the alpha and beta chains of
 RT bovine fibrinogen."
 RL Arch. Biochem. Biophys. 192:27-32(1979).
 RN (7)
 RP SEQUENCE OF 20-49; 243-268 AND 553-580.
 RA Henschen A., Lottepeich F., Topfer-Petersen E., Kehl M., Timpl R.;
 RL (in) Peeters H. (eds.);
 RL Provides of the biological fluids, Proc. 28th colloquium, pp.47-50,
 RL Pergamon Press, Oxford (1980).
 RN (8)
 RP X-RAY CRYSTALLOGRAPHY (4.0 ANGSTROMS) OF 1-390.
 RX MEDLINE=20087206; Pubmed=10618375;
 RA Brown J.H., Volkman N., Jun G., Henschen-Edman A.H., Cohen C.;
 RT "The crystal structure of modified bovine fibrinogen."
 RL Proc. Natl. Acad. Sci. U.S.A. 97:85-90(2000).
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
 CC CONVERTED INTO THE HARD CLOT BY FACTOR XIIIa WHICH CATALYZES THE

CC EPIILON-(GAMMA-GUTTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
CC MONOMERS.

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CC or send an email to license@sib-sib.ch).

DR EMBL: AF095463; AAC67562.1; -

DR PIR: A03117; A03117.

DR PIR: A05294; A05294.

DR PIR: A25715; A25715.

DR PDB: IDEQ: 15-NOV-99.

DR InterPro: IPR002181; Fibrinogen C.

DR PROSITE: PS00514; FIBRIN AG C DOMAIN; PARTIAL.

KW Blood coagulation; Plasma; Glycoprotein; Coiled coil; 3D-structure.

FT PEPTIDE 1 19 FIBRINOPEPTIDE A

FT CHAIN 20 >596 FIBRINOGEN ALPHA CHAIN

FT DOMAIN 102 158 COILED COIL (POTENTIAL)

FT DOMAIN 169 194 COILED COIL (POTENTIAL)

FT DOMAIN 429 432 POLY-THR.

FT SITE 518 523 POLY-SER.

FT SITE 19 20 CLEAVAGE (BY THROMBIN; RELEASE

FT DISULFID 31 31 FIBRINOPEPTIDE A)

FT DISULFID 39 39 INTERCHAIN (WITH C-47) (BY SIMILARITY)

FT DISULFID 48 48 INTERCHAIN (WITH C-95 IN BETA) (BY

FT DISULFID 52 52 INTERCHAIN (WITH C-49 IN GAMMA) (BY

FT DISULFID 164 164 INTERCHAIN (WITH C-106 IN BETA) (BY

FT DISULFID 164 164 INTERCHAIN (WITH C-165 IN GAMMA) (BY

FT DISULFID 168 168 INTERCHAIN (WITH C-223 IN BETA) (BY

FT DISULFID 436 466 BY SIMILARITY

FT CONFLICT 170 170 R -> K (IN REF. 1)

FT CONFLICT 207 208 IL -> LI (IN REF. 1)

FT CONFLICT 219 220 RE -> KK (IN REF. 1)

FT CONFLICT 341 353 MISSING (IN REF. 1)

FT CONFLICT 438 439 KV -> S (IN REF. 2)

FT NON TER 596 596

SO SEQUENCE 596 AA; 65005 MW; 4B74118EF683A26A CRC64;

Query Match Best Local Similarity 80.7%; Score 46; DB 1; Length 596;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPRVERHOSA 11

DB 20 GPRVERHOSA 30

RESULT 4

SM30_HUMAN STANDARD; PRT; 299 AA.

AC 015453;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Serenase marker protein-30 (SMP-30) (Regucalcin) (RC).

GN RGN OR SMP30.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=96004897; PubMed=7548213;

RA Fujita T., Mandel J.L., Shirasawa T., Hino O., Shirai T., Maryama N.;

RT "Isolation of cDNA clone encoding human homologue of senescence

RL marker protein-30 (SMP30) and its location on the X chromosome.";

RP Biochim. Biophys. Acta 1263:249-252(1995).

RC SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA PubMed=1067570;

RT Misawa H., Yamaguchi M.;

RT "Transcript heterogeneity of the human gene for Ca2+-binding protein

RL regucalcin.";

RT Int. J. Mol. Med. 5:283-287(2000).

CC -! FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF ENZYMACTIC ACTIVITY

CC IN THE LIVER. DECREASE OF SMP30 LEADS TO THE DYSREGULATION OF

CC CALCIUM SIGNALING IN THE AGED LIVER.

CC -! SUBCELLULAR LOCATION: CYTOSOL (By similarity).

CC -! SIMILARITY: BELONGS TO THE SMP-30 / CGRI FAMILY.

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CC or send an email to license@sib-sib.ch).

DR EMBL: D31815; BAA06602.1; -

DR EMBL: AB028125; BAA78693.1; -

DR EMBL: AB032064; BAA84082.1; -

DR Genew; HGNC:9899; RGN.

DR MIM; 300212; -

KW Calcium-binding.

SO SEQUENCE 299 AA; 33253 MW; 95BA1C73B7B7635 CRC64;

Query Match Best Local Similarity 66.7%; Score 38; DB 1; Length 299;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PVERHOSA 11

DB 124 PAVLERHQA 133

RESULT 5

Y711_HUMAN STANDARD; PRT; 623 AA.

AC 094819;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical protein KIA0711.

GN KIA0711.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA MEDLINE=99087487; PubMed=9872452;

RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N.,

RA Tanaka A., Kotani H., Nomura N., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. XI.

RT The complete sequences of 100 new cDNA clones from brain which code

RL for large proteins in vitro.";

RL DNA Res. 5:277-286(1998).

CC -! SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.

CC -! SIMILARITY: CONTAINS 4 KETCH REPEATS.

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DR EMBL, AB018254; BA3441.1; -
 DR InterPro: IPR000210; BTB_P0Z.
 DR InterPro: IPR001798; Kelch.
 DR Pfam: PF00651; BTB; 1.
 DR Pfam: PF01344; Kelch; 3.
 DR SMART: SM00225; BTB; 1.
 DR PROSITE: PS50097; BTB; 1.
 KW Hypothetical protein; Repeat.
 FT DOMAIN 140 196 BTB.
 FT REPEAT 311 359 KELCH 1.
 FT REPEAT 360 412 KELCH 2.
 FT REPEAT 413 455 KELCH 3.
 FT REPEAT 458 500 KELCH 4.
 FT REPEAT 500 500
 SQ SEQUENCE 623 AA; 65719 MW; 1044C753A8F478C6 CRC64;

Query Match 66.7%; Score 38; DB 1; Length 623;
 Best Local Similarity 72.7%; Pred. No. 8.4;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GPRVPRHQA 11
 Db 70 GPRVPRHQA 80

RESULT 6
 ID FIBA_RAT STANDARD; PRT; 782 AA.
 AC P06399;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fibrinogen alpha(alpha-E chain precursor [contains: Fibrinopeptide A].
 GN FGA.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Fu Y., Cao Y., Hertzberg K., Grieninger G.;
 RI Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 RN (2)
 RP SEQUENCE FROM N.A. (ALPHA FORM).
 RX MEDLINE=66011580; PubMed=4046033;
 RA Crabtree G.R., Comeau C.M., Fowlkes D.M., Fornace A.J. Jr.,
 RA Malley J.D., Kant J.A.;
 RT "Evolution and structure of the fibrinogen genes. Random insertion of
 RT introns or selective loss?";
 RU J. Mol. Biol. 185:1-19(1985).
 RN (3)
 RP SEQUENCE OF 20-36.
 RA Blomback B., Blomback M., Grondahl N.J.;
 RT "Studies on fibrinopeptides from mammals";
 RU Acta Chem. Scand. 19:1789-1791(1965).
 RN (4)
 RP SEQUENCE OF 458-550 FROM N.A. (ALPHA FORM).
 RC STRAIN=Mistar; TISSUE=Liver;
 RX MEDLINE=8713403; PubMed=3817019;
 RA Sobczak J., Lotfi A.-M., Taroux P., Duguet M.;
 RT "Molecular cloning of mRNA sequences transiently induced during rat
 RT liver regeneration.";
 RU Exp. Cell Res. 169:47-56(1987).
 CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL NODULE.

CC DIVERGING FROM THIS NODULE ARE 2 THREE-CHAIN COILED COILS, WHICH
 CC CONNECT THE CENTRAL NODULE TO THE DISTAL NODULES CONTAINING THE
 CC DISTAL DOMAINS, EXTENDING PAR PERIPHERALLY ARE THE LONG CARBOXYL
 CC ENDS OF THE ALPHA CHAINS.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA-E AND ALPHA, ARE
 CC PRODUCED BY ALTERNATIVE SPLICING. THE ALPHA FORM IS THE
 CC PREDOMINANT FORM.
 CC -1- PTM: THE ALPHA CHAIN IS NOT GLYCOSYLATED.
 CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGENS A AND B FROM ALPHA & BETA
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
 CC CONVERTED INTO THE HARD CLOT BY FACTOR XIIIa WHICH CATALYZES THE
 CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
 CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
 CC MONOMERS.
 CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
 CC -----
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DR EMBL: X86561; CAA60264.1; -
 DR EMBL: X86561; CAA60263.1; -
 DR EMBL: M35601; AAA41158.1; -
 DR PIR: A03119; FGRTA.
 DR HSSP: P02671; 1FZD.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR Pfam: PF00147; fibrinogen_C; 1.
 DR SMART: SM00186; FBG; 1.
 DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; 1.
 DR Blood coagulation; Plasma; Platelet; Signal; Alternative splicing.
 KW SIGNAL 1 19
 FT PEPTIDE 20 36 FIBRINOPEPTIDE A.
 FT CHAIN 20 782 CLEAVAGE (BY THROMBIN; RELEASE
 FT SITE 36 37 FIBRINOPEPTIDE A).
 FT DISULFID 48 48 INTERCHAIN (WITH C-48') (BY SIMILARITY).
 FT DISULFID 56 56 INTERCHAIN (WITH BETA) (BY SIMILARITY).
 FT DISULFID 65 65 INTERCHAIN (WITH C-49 IN GAMMA)
 FT (BY SIMILARITY).
 FT DISULFID 69 69 INTERCHAIN (WITH BETA) (BY SIMILARITY).
 FT DISULFID 181 181 INTERCHAIN (WITH C-165 IN GAMMA)
 FT (BY SIMILARITY).
 FT DISULFID 185 185 INTERCHAIN (WITH BETA) (BY SIMILARITY).
 FT DISULFID 404 434 BY SIMILARITY.
 FT VARSPPLIC 547 550 DCD -> G1HA (IN ISOFORM ALPHA).
 FT VARSPPLIC 551 782 MISSING (IN ISOFORM ALPHA).
 FT CONFLICT 30 34 EAGD -> DEAG (IN REF. 3).
 FT CONFLICT 140 140 Q -> E (IN REF. 2).
 FT CONFLICT 212 212 D -> E (IN REF. 2).
 FT CONFLICT 270 276 ASRGDLP -> LREETYO (IN REF. 2).
 FT CONFLICT 473 473 S -> K (IN REF. 4).
 SQ SEQUENCE 782 AA; 86685 MW; 744834DAE76D34C2 CRC64;

Query Match 66.7%; Score 38; DB 1; Length 782;
 Best Local Similarity 70.0%; Pred. No. 11;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPRVPRHQA 10
 Db 37 GPRVPRHQA 46

RESULT 7
 ID C1W1_HUMAN STANDARD; PRT; 336 AA.
 AC 000180; Q13307;
 DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Potassium channel subfamily K member 1 (inward rectifying potassium
 DE channel protein TWIK-1) (Potassium channel KCNO1).
 GN KCNK1 OR TWIK1 OR HOH01 OR KCNO1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A., FUNCTION, AND MUTAGENESIS OF THR-161.
 RC TISSUE=Kidney;
 RX MEDLINE=96183184; PubMed=8605869;
 RA Lesage F., Guillemare E., Fink M., Duprat F., Lazdunski M., Romey G.,
 RA Barhanin J.;
 RT "TWIK-1, a ubiquitous human weakly inward rectifying K+ channel with a
 RT novel structure.";
 RL EMO J. 15:1004-1011(1996).
 RN (2)
 RP SEQUENCE FROM N.A., AND REVIEW.
 RC TISSUE=Brain;
 RX MEDLINE=98126696; PubMed=9462864;
 RA Goldstein S.A.N., Wang K.-W., Ilan N., Pausch M.H.;
 RT "Sequence and function of the two P domain potassium channels:
 RT implications of an emerging superfamily.";
 RL J. Mol. Med. 76:13-20(1998).
 RN (3)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98026667; PubMed=9362344;
 RA Orias M., Velazquez H., Tung F., Lee G., Desir G.V.;
 RT "Cloning and localization of a double-pore K channel, KCNK1: exclusive
 RT expression in distal nephron segments.";
 RL Am. J. Physiol. 273:F663-F666(1997).
 CC -1- FUNCTION: WEAKLY INWARD RECTIFYING POTASSIUM CHANNEL.
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
 CC -1- TISSUE: HOMODIMER (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: INTEGRAL membrane protein (Potential).
 CC -1- BRAIN AND LOWER LEVELS IN PLACENTA, LUNG, LIVER AND KIDNEY.
 CC -1- MISCELLANEOUS: INHIBITED BY BARIUM, QUININE, QUINIDINE AND
 CC -1- INTERNAL ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
 CC CHANNELS.
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 CC -----
 DR EMBL; U3632; AAB01688.1; -;
 DR EMBL; U76996; AAB97878.1; -;
 DR EMBL; U90065; AAB51147.1; -;
 DR Genew; HGNC:6272; KCNK1.
 DR MIM; 601745; -;
 DR InterPro; IPR003280; K+channel_2pore.
 DR InterPro; IPR001622; K+channel_pore.
 DR InterPro; IPR000636; M-channel_nlg.
 DR InterPro; IPR001779; TWIK1 channel.
 DR Pfam; PF00520; Ion_trans_1.
 DR PRINTS; PR01333; 2FORECHANNEL.
 DR PRINTS; PR01096; TWIK1CHANNEL.
 DR Ionic channel; Transmembrane; Ion transport; Potassium transport;
 KW Glycoprotein.
 FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 21 41 POTENTIAL.
 FT DOMAIN 104 130 PORE-FORMING 1 (POTENTIAL).
 FT TRANSSEM 133 153 POTENTIAL.
 FT DOMAIN 154 177 CYTOPLASMIC (POTENTIAL).
 FT TRANSSEM 178 198 POTENTIAL.
 FT DOMAIN 212 238 PORE-FORMING 2 (POTENTIAL).
 FT TRANSSEM 247 267 POTENTIAL.

FT DOMAIN 268 336 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 95 95 N-LINKED (GLCNAC...) (POTENTIAL).
 FT MUTAGEN 161 161 T->A: NO EFFECT ON CHANNEL ACTIVITY.
 SQ SEQUENCE 336 AA; 38143 MW; 2A4D9501323215D CRC64;
 Query Match 64.9%; Score 37; DB 1; Length 336;
 Best Local Similarity 77.8%; Pred. No. 6.9;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 3 RVERHROSA 11
 DB 12 RIVERHROSA 20
 RESULT 8
 ID CIVI MOUSE STANDARD; PRT; 336 AA.
 AC 009581;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update).
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Potassium channel subfamily K member 1 (inward rectifying potassium
 DE channel protein TWIK-1).
 GN KCNK1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97165959; PubMed=9013852;
 RA Lesage F., Lauritzen I., Duprat F., Reyes R., Fink M., Heurteaux C.,
 RA Lazdunski M.;
 RT "The structure, function and distribution of the mouse TWIK-1 K+
 RT channel.";
 RL FEBS Lett. 402:28-32(1997).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SvC; TISSUE=Liver;
 RX MEDLINE=98218573; PubMed=9559671;
 RA Attigih I., Lesage F., Scimeca J.-C., Carle G.F., Barhanin J.;
 RT "Structure, chromosome localization, and tissue distribution of the
 RT mouse twik K+ channel gene.";
 RL FEBS Lett. 425:310-316(1998).
 CC -1- FUNCTION: WEAK INWARDLY RECTIFYING POTASSIUM CHANNEL.
 CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: INTEGRAL membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST EXPRESSION IN BRAIN,
 CC KIDNEY, THYROID, SALIVARY GLAND, ADRENAL GLAND, PROSTATE,
 CC EPIDIDYMIS, UTERUS, PITUITARY, PANCREAS, SMOOTH MUSCLE, TESTIS AND
 CC OVARY. VERY LOW LEVELS IN LUNG, AORTA, LIVER, HEART, SKELETAL
 CC MUSCLE, THYMUS AND SPLEEN. IN THE BRAIN, HIGHEST EXPRESSION IN
 CC CEREBELLAR GRANULE CELLS, BRAINSTEM, HIPPOCAMPUS AND CEREBRAL
 CC CORTIX.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSION DETECTED AS EARLY AS 7 DAYS POST
 CC CONCEPTION. EXPRESSION INCREASES FROM 2-8 DAYS AFTER BIRTH AND
 CC STABILIZES AFTER DAY 8.
 CC -1- MISCELLANEOUS: INHIBITED BY QUININE, BARIUM, AND INTERNAL
 CC ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.
 CC -1- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
 CC CHANNELS.
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 CC -----
 DR EMBL; AF033017; AAC16973.1; -;

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DR MGD; MGI:109322; Kcnk1.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR000636; M-channel_nlg.
DR InterPro; IPR001779; TWIK1_channel.
DR Pfam; PF00520; Ion_trans; I.
DR PRINTS; PRO133; 2PORECHANNEL.
DR PRINTS; PRO1096; TWIK1CHANNEL.
KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW Glycoprotein.
FT DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 21 41 POTENTIAL.
FT DOMAIN 104 130 PORE-FORMING 1 (POTENTIAL):
FT TRANSSEM 133 153 POTENTIAL.
FT DOMAIN 154 177 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 178 198 POTENTIAL.
FT DOMAIN 212 238 PORE-FORMING 2 (POTENTIAL).
FT TRANSSEM 247 267 POTENTIAL.
FT DOMAIN 268 336 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 336 AA; 38275 MW; A996060A1826FP4 CRC64;

Query Match 64.9%; Score 37; DB 1; Length 336;
Best Local Similarity 77.8%; Pred. No. 6.9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 3 RVERHOSA 11
Db 12 RIVERHSA 20

RESULT 9
YNI1_CABEL STANDARD; PRT; 108 AA.
ID YNI1_CABEL STANDARD; PRT; 108 AA.
AC P91375; 1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE Hypothetical 12.1 kDa protein K11H12.1 in chromosome IV.
GN K11H12.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peleodermidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Brdshaw H.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE BOLA / YRBA FAMILY.
CC -----
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CC -----
CC
DR EMBL; U88168; AAC24398.1; -
DR WormPep; K11H12.1; CE12146.
DR InterPro; IPR002634; BOLA.
DR Pfam; PF01723; BOLA; 1.
KW Hypothetical protein.
SQ SEQUENCE 108 AA; 12146 MW; 4199A3C09C20ACF2 CRC64;

Query Match 63.2%; Score 36; DB 1; Length 108;
Best Local Similarity 66.7%; Pred. No. 3.3;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GPRVERHQ 9
Db 56 GKRVIERHR 64

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RESULT 10
PRIM_ECOLI STANDARD; PRT; 561 AA.
ID PRIM_ECOLI STANDARD; PRT; 561 AA.
AC P02923; F02922;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DNA primase (EC 2.7.7.-).
GN DNAG OR DNAP OR PARB OR B3066 OR Z4419 OR ECS3949.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83129424; PubMed=6186393;
RA Burton Z.F., Gross C.A., Watanabe K.K., Burgess R.R.;
RT "The operon that encodes the sigma subunit of RNA polymerase also
RT encodes ribosomal protein S21 and DNA primase in E. coli K12."
RL Cell 32:335-349(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83014926; PubMed=6750604;
RA Smiley B.L., Lupski J.R., Svec P.S., McMacken R., Godson G.N.;
RT "Sequences of the Escherichia coli dnaG primase gene and regulation
RT of its expression."
RL Proc. Natl. Acad. Sci. U.S.A. 79:4550-4554(1982).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.D.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1232-1274(1997).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / EDL933 / ATCC 700927;
RC MEDLINE=21074935; PubMed=11206551;
RX Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobbeck E.J., Davis N.W., Lim A., DiMantia E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533(2001).
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=O157:H7 / RIMD 0509952;
RC MEDLINE=21156231; PubMed=11258796;
RX Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kihara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12."
RL DNA Res. 8:11-22(2001).
RN [6]
RP ZINC-BINDING.
RX MEDLINE=92379087; PubMed=1511009;
RA Stamford N.P.J., Lilly P.E., Dixon N.E.;
RT "Enriched sources of Escherichia coli replication proteins. The dnaG
RT primase is a zinc metalloprotein."
RL Biochim. Biophys. Acta 1132:17-25(1992).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 109-429.
RX MEDLINE=20334715; PubMed=10873470;

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RA Podobnik M., McInerney P., O'Donnell M., Kuriyan J.;
RT "A TOPPRIM domain in the crystal structure of the catalytic core of
RT Escherichia coli primase confirms a structural link to DNA
RT topoisomerases."
CC J. Mol. Biol. 300:353-362(2000).
CC
CC -1- FUNCTION: DNA PRIMASE IS THE POLYMERASE THAT SYNTHESIZES SMALL
CC RNA PRIMERS FOR THE OKAZAKI FRAGMENTS ON BOTH TEMPLATE STRANDS AT
CC REPLICATION FORKS DURING CHROMOSOMAL DNA SYNTHESIS.
CC -1- COPACITOR: BINDS ONE ZINC ION PER MOLECULE.
CC -1- SUBUNIT: MONOMER.
CC -1- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITIONS 106
CC TO 169 DUE TO FRAMESHIFTS.
CC
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CC -----
DR EMBL; J01687; AAA24600.1; -
DR EMBL; V00274; CAA23531.1; ALT_FRAME.
DR EMBL; U28379; AAA89146.1; -
DR EMBL; AE000388; AAC76102.1; -
DR EMBL; AE005536; AAG58200.1; -
DR EMBL; AF002564; BAB37372.1; -
DR PIR; A03423; RYEC2.
DR PIR; A03422; RYEC.
DR PDB; 1EON; 30-JUN-00.
DR EC02DBASE; G060.0; 6TH EDITION.
DR Ecogen; Egi0239; dnaG.
DR InterPro; IPR002936; DNAPrim_toprim.
DR InterPro; IPR002694; Znf_CHC2.
DR Pfam; PF01751; Toprim; 1.
DR Pfam; PF01807; zf-CHC2; 1.
DR ProDom; PD002988; Znf_CHC2; 1.
DR SMART; SM00493; TOPRIM; 1.
DR SMART; SM00400; Znf_CHC2; 1.
DR Transfaser; DNA replication; DNA-directed RNA polymerase; Primosome;
KW Zinc-finger; Zinc; Metal-binding; Complete proteome; 3D-structure.
FT ZN_FING 40 64
FT SEQUENCE 581 AA; 65564 MW; 294CF020E7B45D94 CRC64;

Query Match 63.2%; Score 36; DB 1; Length 581;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPRVVERHQ 9
DB 104 GPSQIERHQ 112

RESULT 11
SM30_MOUSE STANDARD; PRT; 299 AA.
AC Q64374; Q60944;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Senescence marker protein-30 (SMP-30) (Regucalcin) (RC).
GN RGN OR SMP30.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Liver;
RA MEDLINE=96328264; PubMed=8765750;
RA Fujita T., Shirasawa T., Maruyama N.;
RT "Isolation and characterization of genomic and cDNA clones encoding
RT mouse senescence marker protein-30 (SMP30).";

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RL Biochim. Biophys. Acta 1308:49-57(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=97422495; PubMed=9278263;
RA Murata T., Yamaguchi M.;
RT "Molecular cloning of the cDNA coding for regucalcin and its mRNA
RT expression in mouse liver: the expression is stimulated by calcium
RT administration."
RL Mol. Cell. Biochem. 173:127-133(1997).
CC -1- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF ENZYMAIC ACTIVITY
CC IN THE LIVER. DECREASE OF SMP30 LEADS TO THE DYSREGULATION OF
CC CALCIUM SIGNALING IN THE AGED LIVER.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: MAINLY PRESENT IN THE LIVER. WEAK EXPRESSION
CC WAS FOUND IN THE BRAIN AND LUNG, NOT FOUND IN THE KIDNEY.
CC -1- DEVELOPMENTAL STAGE: PROTEIN AMOUNTS IN LIVER DECREASE
CC SIGNIFICANTLY WITH AGE.
CC -1- SIMILARITY: BELONGS TO THE SMP-30 / CGR1 FAMILY.
CC -----
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CC -----
DR EMBL; U28937; AAC52721.1; -
DR EMBL; U32170; AAD03478.1; -
DR EMBL; D86217; BAA13046.1; -
DR SWISS-2DPAGE; Q64374; MOUSE.
DR MGD; MG1:108024; Rgn.
KW Calcium-binding.
FT SEQUENCE 299 AA; 33407 MW; DAD5EF618311977 CRC64;

Query Match 61.4%; Score 35; DB 1; Length 299;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PVRVERHQA 11
DB 124 PAVLERRHQS 133

RESULT 12
SM30_RABIT STANDARD; PRT; 299 AA.
AC Q9TJ06;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Senescence marker protein-30 (SMP-30) (Regucalcin) (RC).
GN RGN OR SMP30.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20351777; PubMed=10891565;
RA Misawa H., Yamaguchi M.;
RT "The gene of Ca2+-binding protein regucalcin is highly conserved in
RT vertebrate species."
RL Int. J. Mol. Med. 6:191-196(2000).
CC -1- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF ENZYMAIC ACTIVITY
CC IN THE LIVER. DECREASE OF SMP30 LEADS TO THE DYSREGULATION OF
CC CALCIUM SIGNALING IN THE AGED LIVER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SMP-30 / CGR1 FAMILY.
CC -----
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CC -----
 CC DR EMBL; AB035445; BAA88079.1; -
 CC KM Calcium-binding.
 CC SEQUENCE 299 AA; 33108 MW; A8F94AD596A0C68 CRC64;

Query Match 61.4%; Score 35; DB 1; Length 299;
 Best Local Similarity 60.0%; Pred. No. 15;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRVERHOSA 11
 Db 124 PAVLHROGS 133

RESULT 13
 SM30 RAT
 ID SM30 RAT STANDARD; PRT; 299 AA.
 AC Q03336; Q63496;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Senescence marker protein-30 (SMP-30) (Regucalcin) (RC).
 GN RGN OR SMP30.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RC STRAIN=Wistar; TISSUE=Liver;
 RX MEDLINE=93041931; PubMed=1420310;
 RA Fujita T., Shizsawa T., Uchida K., Maruyama N.;
 RT "Isolation of cDNA clone encoding rat senescence marker protein-30
 RT (SMP30) and its tissue distribution";
 RL Biochim. Biophys. Acta 1132:297-305(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Liver;
 RX MEDLINE=9351639; PubMed=8348951;
 RA Shimokawa N., Yamaguchi M.;
 RT "Molecular cloning and sequencing of the cDNA coding for a calcium-
 RT binding protein regucalcin from rat liver";
 RL FEBS Lett. 327:251-255(1993).
 RN [3]
 RP SEQUENCE OF 117-299 FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
 RX MEDLINE=96150990; PubMed=8569761;
 RA Shimokawa N., Matsuda Y., Yamaguchi M.;
 RT "Genomic cloning and chromosomal assignment of rat regucalcin gene";
 RL Mol. Cell. Biochem. 151:157-163(1995).
 RN [4]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=96386712; PubMed=8794449;
 RA Fujita T., Shizsawa T., Uchida K., Maruyama N.;
 RT "Gene regulation of senescence marker protein-30 (SMP30): coordinated
 RT up-regulation with tissue maturation and gradual down-regulation
 RT with aging";
 RL Mech. Ageing Dev. 87:219-229(1996).
 CC -1- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF ENZYMAIC ACTIVITY
 CC IN THE LIVER. DECREASE OF SMP30 LEADS TO THE DYSREGULATION OF
 CC CALCIUM SIGNALING IN THE AGED LIVER.
 CC -1- SUBCELLULAR LOCATION: CYTOSOLASMIC.
 CC -1- TISSUE SPECIFICITY: HEPATOCYTES AND RENAL PROXIMAL TUBULAR
 CC EPITHELIUM.
 CC -1- DEVELOPMENTAL STAGE: IN LIVER, THE FIRST PEAK OF EXPRESSION WAS
 CC FOUND IN 5-DAY-OLD NEONATES. EXPRESSION INCREASES FROM DAY 7 AND
 CC REACHES A PLATEAU AT DAY 10. 3-6.5 MONTH-OLD ADULTS EXPRESS ABOUT A

CC THIRD THE AMOUNT OF NEONATES LEVEL. IN KIDNEY, EXPRESSION
 CC INCREASES FROM DAY 21 AND REACHES A MAXIMAL LEVEL AT DAY 35,
 CC REMAINS HIGH UNTIL 3 MONTHS OF AGE.
 CC -1- PTM: THE N-TERMINUS IS BLOCKED.
 CC -1- SIMILARITY: BELONGS TO THE SMP-30 / CGR1 FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).

CC -----
 CC DR EMBL; X69021; CAA48786.1; -
 CC DR EMBL; D38467; BAA07490.1; -
 CC DR EMBL; D31662; BAA06507.1; -
 CC DR PIR; S27203; S27203.
 CC KM Calcium-binding.
 CC FT CONFLICT 148 N -> D (IN REF. 1).
 CC SEQUENCE 299 AA; 33389 MW; E3CFED3FFCAE4E98 CRC64;

Query Match 61.4%; Score 35; DB 1; Length 299;
 Best Local Similarity 60.0%; Pred. No. 15;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRVERHOSA 11
 Db 124 PAVLHROGS 133

RESULT 14
 HOXO ALCEU
 ID HOXO ALCEU STANDARD; PRT; 161 AA.
 AC P21910;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Hydrogenase expression/formation protein hoxo.
 GN HOXO.
 OS Alcaligenes eutrophus (Ralstonia eutropha).
 OG Alkalimdia megaplasmid pHG1.
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
 OC Ralstonia.
 OX NCBI_TaxID=510;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H16 / DSM 428 / ATCC 17699;
 RX MEDLINE=93015670; PubMed=1383192;
 RA Kortluke C., Horstmann K., Schwartz E., Rohde M., Binsack R.,
 RA Friedlrich B.;
 RT "A gene complex coding for the membrane-bound hydrogenase of
 RT Alcaligenes eutrophus H16";
 RL J. Bacteriol. 174:6277-6289(1992).
 CC -1- SIMILARITY: BELONGS TO THE HUPG/HYAE FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).

CC -----
 CC DR EMBL; M96435; AAA16467.1; -
 CC DR PIR; G43255; G43255.
 CC KM Plasmid.
 CC SEQUENCE 161 AA; 17719 MW; 5A46346F7953E80F CRC64;

Query Match 59.6%; Score 34; DB 1; Length 161;
 Best Local Similarity 66.7%; Pred. No. 12;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 RVERHQSA 11
 Db 24 RLECHQAA 32

```

RESULT 15
PNB1_PSEAE
ID PNB1_PSEAE STANDARD; PRT: 399 AA.
AC Q9HUP4;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Nicotinate phosphoribosyltransferase 1 (EC 2.4.2.11) (NAPRTase 1).
GN PNCB1 OR PA4919.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
CC Pseudomonas.
OK NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=2043737; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Salter M.H., Hancock R.E.W., Lory S., Olson M.V.,
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen."
RL Nature 406:959-964 (2000).
CC -|- CATALYTIC ACTIVITY: Nicotinate D-ribonucleotide + diphosphate =
CC -|- nicotinate + 5-phospho-alpha-D-ribose 1-diphosphate.
CC -|- PATHWAY: NAD biosynthesis; nicotinamide to NAMN; second step.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
CC -|- SIMILARITY: BELONGS TO THE NAPRTASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE004905; AAG08304.1;
KW Pyridine nucleotide biosynthesis; Transferase; Glycosyltransferase;
KW Complete proteome.
SQ SEQUENCE 399 AA; 46095 MW; 49B2266CF47346DE CRC64;
Query Match 59.6%; Score 34; DB 1; Length 399;
Best Local Similarity 54.5%; Pred. No. 32;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
OY 1 GPRVVERHQSA 11
Db 234 GPRLVDSQQA 244

```

Search completed: June 27, 2003, 17:17:08
 Job time : 9.7 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 17:14:41 ; Search time 26.4 Seconds

(without alignments)
85.853 Million cell updates/sec

Title: US-10-019-439-1

Perfect score: 57

Sequence: 1 GPRVRRHQA 11

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mmc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_proteic:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	218	4	Q8W76
2	53	93.0	557	11	Q99K47
3	41	71.9	105	13	Q919N1
4	37	64.9	323	10	Q9LDE1
5	37	64.9	336	11	Q922T2
6	37	64.9	336	11	Q99L99
7	37	64.9	336	11	Q8RA54
8	36	63.2	347	16	Q9FC35
9	36	63.2	552	10	Q9CEA4
10	35	61.4	65	2	Q53379
11	35	61.4	215	11	Q9D7V2
12	35	61.4	299	11	Q925W3
13	35	61.4	338	5	Q9VC74
14	35	61.4	368	17	Q8TXJ9
15	35	61.4	372	5	Q95V11
16	35	61.4	428	16	Q9X0D1

17	35	61.4	481	5	Q95CP9	Q95CP9 drosophila
18	35	61.4	481	5	Q9VEP6	Q9VEP6 drosophila
19	35	61.4	493	16	Q8R958	Q8R958 thermomater
20	35	61.4	590	10	Q8S4W7	Q8S4W7 vitis vinif
21	35	61.4	632	10	Q8VZ40	Q8VZ40 arabidopsis
22	35	61.4	639	10	Q9SV34	Q9SV34 arabidopsis
23	35	61.4	829	16	Q9BDP8	Q9BDP8 rhizobium
24	35	61.4	885	16	Q8XTK5	Q8XTK5 ralestonia
25	35	61.4	1390	5	Q9N6B9	Q9N6B9 leishmania
26	34.5	60.5	121	16	Q8UEF2	Q8UEF2 agrobacteri
27	34	59.6	67	16	Q99V14	Q99V14 staphylococ
28	34	59.6	78	16	Q8XV77	Q8XV77 ralestonia
29	34	59.6	165	10	Q8S3Y9	Q8S3Y9 sorghum bic
30	34	59.6	218	10	Q9ZTC6	Q9ZTC6 arabidopsis
31	34	59.6	236	4	Q9BT48	Q9BT48 homo sapien
32	34	59.6	292	3	Q9P5Y3	Q9P5Y3 neurospora
33	34	59.6	307	10	Q9FGY3	Q9FGY3 arabidopsis
34	34	59.6	333	4	Q9NRN7	Q9NRN7 homo sapien
35	34	59.6	346	17	Q97Z17	Q97Z17 sulfolobus
36	34	59.6	399	16	Q9HUP4	Q9HUP4 pseudomonas
37	34	59.6	413	4	Q9H8J9	Q9H8J9 homo sapien
38	34	59.6	471	2	Q8RK23	Q8RK23 pseudomonas
39	34	59.6	529	16	Q8G318	Q8G318 mycobacteri
40	34	59.6	531	16	Q8VKA7	Q8VKA7 mycobacteri
41	34	59.6	567	10	Q24604	Q24604 dioscortea
42	34	59.6	720	10	Q94GL4	Q94GL4 oryza sativ
43	34	59.6	866	10	Q8S2P1	Q8S2P1 oryza sativ
44	34	59.6	885	5	Q9VP26	Q9VP26 drosophila
45	34	59.6	950	16	Q9A4B3	Q9A4B3 caulobacter

ALIGNMENTS

RESULT 1

Q8W76 PRELIMINARY; PRT; 218 AA.

AC Q8W76; 01-MAR-2002 (TREMUREL. 20, Created)

DT 01-MAR-2002 (TREMUREL. 20, Last sequence update)

DT 01-MAR-2002 (TREMUREL. 20, Last annotation update)

DE Similar to fibrinogen, A alpha polypeptide.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=LIVER;

RA Strauberg R.;

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL, BC020764; AAH20764.1; -; 36D756A811EA94A CRC64;

SQ SEQUENCE 218 AA; 24695 MW; 36D756A811EA94A CRC64;

Query Match 100.0%; Score 57; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRVRRHQA 11

Db 36 GPRVRRHQA 46

RESULT 2

Q9K47 PRELIMINARY; PRT; 557 AA.

AC Q9K47; 01-JUN-2001 (TREMUREL. 17, Created)

DT 01-JUN-2001 (TREMUREL. 17, Last sequence update)

DT 01-DEC-2001 (TREMUREL. 19, Last annotation update)

DE Fibrinogen A alpha polypeptide.

GN FGA.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC005467; AAH05467.1; -
 DR HSSP: P02671; 1FZA.
 DR MGP: MGI:131676; Fga.
 SQ SEQUENCE 557 AA; 61325 MW; C47F496D1BA432DE CRC64;
 Query Match 93.0%; Score 53; DB 11; Length 557;
 Best Local Similarity 100.0%; Pred. No. 0.046;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GPRVERHQOS 10
 Db 37 GPRVERHQOS 46
 RESULT 3
 ID Q919N1 PRELIMINARY; PRT; 105 AA.
 AC Q919N1;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Dap1a.
 GN DAPIA.
 OS Brachydanio rerio (Zebrafish) (Zebra danio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NC NCB1_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20373792; PubMed=10917738;
 RA Inohara N., Nunez G.;
 RT "Genes with homology to mammalian apoptosis regulators identified in zebrafish."
 RL Cell Death Differ. 7:509-510(2000).
 DR EMBL: AF231127; AAF66957.1; -
 SQ SEQUENCE 105 AA; 11367 MW; 715DD7AF236F5D56 CRC64;
 Query Match 71.9%; Score 41; DB 13; Length 105;
 Best Local Similarity 63.6%; Pred. No. 1.9;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 GPRVERHQSA 11
 Db 23 GMRIVQKHQA 33
 RESULT 4
 ID Q9LDEL PRELIMINARY; PRT; 323 AA.
 AC Q9LDEL;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Putative transcription factor MYB108 (Myb-related protein, putative).
 GN MYB108 OR F5B6.18.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
 NC NCB1_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Stracke R., Weishaar B.;

RT "MYB transcription factor gene nomenclature in Arabidopsis thaliana";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
 RA Maiti R., Rongming C.M., Koo H., Fujii C.Y., Uteback T.R.,
 RA Banstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RT "Arabidopsis thaliana chromosome 3 BAC F56 genomic sequence."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 2 MYB-LIKE DOMAINS.
 DR EMBL: AF262733; AAF72668.1; -
 DR EMBL: AC020580; AAG51322.1; -
 DR HSSP: P01103; IPOM.
 DR InterPro: IPR001005; Myb_DNA_binding.
 DR Pfam: PF00249; myb_DNA-binding; 2.
 DR SMART: SM00395; SANT; 2.
 DR PROSITE: PS00037; MYB_1; UNKNOWN_1.
 DR PROSITE: PS00334; MYB_2; 1.
 DR PROSITE: PS50090; MYB_3; 2.
 DR DNA-binding; Nuclear protein.
 SQ SEQUENCE 323 AA; 37019 MW; BB0FF0A362192165 CRC64;
 Query Match 64.9%; Score 37; DB 10; Length 323;
 Best Local Similarity 80.0%; Pred. No. 37;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 2 PRVERHQSA 11
 Db 145 PLVERHQSA 154
 RESULT 5
 ID Q9Z2T2 PRELIMINARY; PRT; 336 AA.
 AC Q9Z2T2;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Putative potassium channel TWIK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCB1_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gan L., Joiner W.J., Quinn A.M., Wang L.-Y., Hughes T.,
 RA Kaczmarek L.K.;
 RT "Cloning and localization of rTWIK, a putative potassium channel with two P domains."
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF022819; AAD09336.1; -
 DR InterPro: IPR003280; K-channel_2pore.
 DR InterPro: IPR001622; K-channel_pore.
 DR InterPro: IPR000636; K-channel_nlg.
 DR InterPro: IPR001779; TWIK1_channel.
 DR Pfam: PF00520; ion_trans; 1.
 DR PRINTS: PRO133; 2PORECHANNEL.
 DR PRINTS: PRO1096; TWIK1CHANNEL.
 DR PRINTS: PRO1587; TWIK2CHANNEL.
 DR PRINTS: PRO1586; TWIKCHANNEL.
 KW Ionic channel.
 SQ SEQUENCE 336 AA; 38228 MW; 5E78031947D75DE6 CRC64;
 Query Match 64.9%; Score 37; DB 11; Length 336;
 Best Local Similarity 77.8%; Pred. No. 39;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 3 RVERHQSA 11
 Db 12 RLVERHRSQA 20

```

RESULT 6
Q99L99          PRELIMINARY;      PRT;      336 AA.
ID  Q99L99;
AC  Q99L99;
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE  Potassium channel, subfamily K, member 1.
GN  KCNK1.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Strausberg R.;
RL  Submitted (FEBS-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC003729; AAI03729.1; -.
DR  MGI; MGI:109322; Kcnk1.
DR  InterPro; IPR003280; K+channel_2pore.
DR  InterPro; IPR001622; K+channel_pore.
DR  InterPro; IPR000636; M+channel_nlg.
DR  InterPro; IPR001779; TWIK1_channel.
DR  Pfam; PF00520; Ion_trans_1.
DR  PRINTS; PRO1333; 2PORECHANNEL.
DR  PRINTS; PRO1096; TWIK1CHANNEL.
DR  PRINTS; PRO1587; TWIK2CHANNEL.
DR  PRINTS; PRO1586; TWIKCHANNEL.
SQ  SEQUENCE 336 AA; 38201 MW; 76B7FD5361A6216C CRC64;

Query Match          64.9%; Score 37; DB 11; Length 336;
Best Local Similarity 77.8%; Pred. No. 39;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy  3 RYVERHOSA 11
    |||||:|
Db  12 RLYVERHOSA 20

RESULT 7
Q8R454          PRELIMINARY;      PRT;      336 AA.
ID  Q8R454;
AC  Q8R454;
DT  01-JUN-2002 (TrEMBLrel. 21, Created)
DT  01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  Potassium channel TWIK-1.
GN  KCNK1.
OS  Cavia porcellus (Guinea pig).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX  NCBI_TaxID=10141;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Derst C., Rajan S., Preisig-Mueller R.;
RT  "Cloning and sequencing of guinea pig TWIK channels.";
RT  Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AY075096; AAL82795.1; -.
SQ  SEQUENCE 336 AA; 38102 MW; 299B69159D7F5B2A CRC64;

Query Match          64.9%; Score 37; DB 11; Length 336;
Best Local Similarity 77.8%; Pred. No. 39;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy  3 RYVERHOSA 11
    |||||:|
Db  12 RLYVERHOSA 20

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AC  Q9FC35;
DT  01-MAR-2001 (TrEMBLrel. 16, Created)
DT  01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  Putative delta fatty acid desaturase.
GN  SC07048 OR SC4G1.14C.
OS  Streptomyces coelicolor.
OC  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC  Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
OX  NCBI_TaxID=1902;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=A3(2);
RA  Brown S.P.;
RL  Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=A3(2);
RA  Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL  Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN=A3(2);
RX  MEDLINE=97000351; Pubmed=8843436;
RA  Redenbach M., Kleiser H.M., Denapate D., Eichner A., Cullum J.,
RA  Knasht H., Hopwood D.A.;
RT  "A set of ordered cosmids and a detailed genetic and physical map for
RT  the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL  Mol. Microbiol. 21:77-96(1996).
[4]
RP  SEQUENCE FROM N.A.
RC  STRAIN=A3(2) / M145;
RA  Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA  Thornton N.R., James K.D., Harris D.E., Quail M.A., Kleiser H.,
RA  Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA  Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA  Huang C.-H., Kleiser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA  Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA  Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA  Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
RA  Hopwood D.A.;
RT  "Complete genome sequence of the model actinomycete Streptomyces
RT  coelicolor A3(2).";
RL  Nature 417:141-147(2002).
DR  EMBL; AL391039; CA001546.1; -.
DR  InterPro; IPR001225; FA_desaturase.
DR  Pfam; PF00487; FA_desaturase; 1.
DR  ProDom; PD001081; FA_desaturase; 1.
SQ  SEQUENCE 347 AA; 37990 MW; 201E2D716CB46419 CRC64;

Query Match          63.2%; Score 36; DB 16; Length 347;
Best Local Similarity 70.0%; Pred. No. 63;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy  2 PRYVERHOSA 11
    |||||:|
Db  159 PRYVERHOSA 168

RESULT 9
Q9C6A4          PRELIMINARY;      PRT;      552 AA.
ID  Q9C6A4;
AC  Q9C6A4;
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT  01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE  Hypothetical 61.0 kDa protein.
GN  P9E11.8.
OS  Arabidopsis thaliana (Mouse-ear cress).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC  eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX  NCBI_TaxID=3702;

```

RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA:
 RA MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federpiet N.A., Kaul S.,
 RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway R.F., Creasy T.H., Dewar K.,
 RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremetskaia I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
 RA Miltischer J., Miranda M., Nguyen M., Nieman W.C., Osborne B.I.,
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sano H., Salzer S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Uterback T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 thaliana."
 RL Nature 408:816-820(2000).
 DR EMBL: AC079678; AAG51875.1;
 DR InterPro: IPR001798; Keln.
 DR Pfam: PF01344; Keln; 5.
 KW Hypothetical protein.
 SQ SEQUENCE 552 AA; 60960 MW; C43692695EDDC56 CRC64;

Query Match 63.2%; Score 36; DB 10; Length 552;
 Best Local Similarity 63.6%; Pred. No. 1e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 121 GPRVREHQA 11
 121 GPRVREHQA 131

RESULT 10
 OS3379 PRELIMINARY; PRT; 65 AA.
 ID OS3379
 AC OS3379;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE URF 5.
 OS *Synechococcus* sp. (strain PCC 6716).
 OC Bacteria; Cyanobacteria; Chroococcales; *Synechococcus*.
 OX NCBI_TaxID=32048;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=6716;
 RX MEDLINE=93371369; PubMed=8363578;
 RA van Waikaven H.S., Lutter R., Walker J.E.,
 RT "Organization and sequences of genes for the subunits of ATP synthase
 in the thermophilic cyanobacterium *Synechococcus* 6716."
 RL Biochem. J. 294:239-251(1993).
 DR EMBL: X70431; CAA49881.1;
 FT CHAIN
 SQ SEQUENCE 65 AA; 7561 MW; A1BFL320457BCA48 CRC64;

Query Match 61.4%; Score 35; DB 2; Length 65;
 Best Local Similarity 45.5%; Pred. No. 18;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Db 17 GPRVREHQA 11
 17 GPRVREHQA 27

RESULT 11
 OS3379 PRELIMINARY; PRT; 215 AA.
 ID OS3379
 AC OS3379;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE URF 5.
 OS *Synechococcus* sp. (strain PCC 6716).
 OC Bacteria; Cyanobacteria; Chroococcales; *Synechococcus*.
 OX NCBI_TaxID=32048;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=6716;
 RX MEDLINE=93371369; PubMed=8363578;
 RA van Waikaven H.S., Lutter R., Walker J.E.,
 RT "Organization and sequences of genes for the subunits of ATP synthase
 in the thermophilic cyanobacterium *Synechococcus* 6716."
 RL Biochem. J. 294:239-251(1993).
 DR EMBL: X70431; CAA49881.1;
 FT CHAIN
 SQ SEQUENCE 65 AA; 7561 MW; A1BFL320457BCA48 CRC64;

AC OS3379
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE 2210402C18Rik protein.
 GN 2210402C18Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=STOMACH;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Kawata T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Giesi C., King B., Kocikova H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiraldi L.M., Scuderi P., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Botfeill D., Bouung A.N., Carninci P., de Bonaldo M.F.,
 RA Brownstein S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima T., Mazzarelli J., Mombarts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whiteaker C., Wilming L.,
 RA Wyrshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlschki S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL: AK008800; BAB25902.1;
 DR MGI: 1917332; 2210402C18Rik.
 DR InterPro: IPR002482; LysM.
 DR Pfam: PF01476; LysM; 1.
 DR SMART: SM00257; LysM; 1.
 SQ SEQUENCE 215 AA; 23765 MW; DC011B368AD1B976 CRC64;

Query Match 61.4%; Score 35; DB 11; Length 215;
 Best Local Similarity 75.0%; Pred. No. 61;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 63 GARVIERH 70
 63 GARVIERH 70

RESULT 12
 OS3379 PRELIMINARY; PRT; 299 AA.
 ID OS3379
 AC OS3379;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Regucalcin.
 OS *Rattus norvegicus* (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; *Rattus*.
 OX NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=6716;
 RX MEDLINE=93371369; PubMed=8363578;
 RA van Waikaven H.S., Lutter R., Walker J.E.,
 RT "Organization and sequences of genes for the subunits of ATP synthase
 in the thermophilic cyanobacterium *Synechococcus* 6716."
 RL Biochem. J. 294:239-251(1993).
 DR EMBL: X70431; CAA49881.1;
 FT CHAIN
 SQ SEQUENCE 299 AA; 33390 MW; 5D8F2D95FCA4EE35 CRC64;

Query Match 61.4%; Score 35; DB 11; Length 299;
 Best Local Similarity 60.0%; Pred. No. 86;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRVERHQSA 11
Db 124 PAVLERHGS 133

RESULT 13

09VG74 PRELIMINARY; PRT; 338 AA.
ID 09VG74
AC 09VG74
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE CG5232 protein.
GN NEUSAC OR CG5232.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abirl J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkov D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dubin K.J., Evangelista C.C., Ferrara C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaisi M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Ling Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AB003695; AAF54811.1;
DR FlyBase: FBgn0038045; Neusac.
DR InterPro: IPR000029; AntifreezeIII.
DR InterPro: IPR004144; Neub.
DR Pfam: PF01354; Antifreeze; 1.
DR Pfam: PF03102; Neub; 1.
SQ SEQUENCE 338 AA; 37535 MW; 95F03C4FE42956C2 CRC64;

Query Match 61.4%; Score 35; DB 5; Length 338;
Best Local Similarity 75.0%; Pred. No. 97;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPRVERH 8
Db 194 GARVERH 201

RESULT 14

08TXJ9 PRELIMINARY; PRT; 368 AA.
ID 08TXJ9
AC 08TXJ9
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE RI01-like serine/threonine protein kinase fused to an N-terminal
DE DNA-binding HTH domain.
GN MK0674.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA Shekerbina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natale D.A., Rogozin I.B., Tatunov R.L., Wolf Y.I., Stetter K.O.,
RA Malynk A.G., Koonin E.V., Kozlyavkin S.A.,
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal mechanogens."
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
DR EMBL: AE010360; AAM01889.1;
KW Kinase; Serine/threonine-protein kinase; Complete proteome.
SQ SEQUENCE 368 AA; 42423 MW; E7C4809608E7578 CRC64;

Query Match 61.4%; Score 35; DB 17; Length 368;
Best Local Similarity 54.5%; Pred. No. 11e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPRVERHQSA 11
Db 184 GPRVHNHAVA 194

RESULT 15

09SVY1 PRELIMINARY; PRT; 372 AA.
ID 09SVY1
AC 09SVY1
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Neusac synthase.
GN NEUSAC OR CG5232.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]

RP SEQUENCE FROM N.A.
RC STRAIN=OREGON R;
RA Kim K., Lawrence S.M., Park J., Pitts L., Vann W.F., Betendough M.J.,
RA Palter K.B.;
RT "Expression of a functional Drosophila melanogaster N-acetylneuraminic
RT acid (Neusac) phosphate synthase gene: Evidence for endogenous static
RT acid biosynthetic ability in insects."
RL Glycobiology 0:0-0(2001).
DR EMBL: AF397531; AAK92125.1;
DR FlyBase: FBgn0038045; Neusac.
DR InterPro: IPR000029; Antifreeze.
DR InterPro: IPR004144; Neub.
DR Pfam: PF01354; Antifreeze; 1.
DR Pfam: PF03102; Neub; 1.

SQ SEQUENCE 372 AA; 41218 MW; 9C7ADB0567422F3E CRC64;
Query Match 61.4%; Score 35; DB 5; Length 372;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GPRVVERH 8
|:||||
Db 228 GARTVERH 235

Search completed: June 27, 2003, 17:18:03
Job time : 28.4 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 17:12:16 ; Search time 33.55 Seconds

(without alignments)
43.689 Million cell updates/sec

Title: US-10-019-439-1

Perfect score: 57

Sequence: 1 GPRVERHQSA 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 0%

Listing first 45 summaries

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23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	57	100.0	36	22	Residues 36-46 of
2	57	100.0	36	19	GP11b/IIIA receptor
3	57	100.0	36	13	Fibrin derived pep
4	57	100.0	36	14	GP IIb/IIIa receptor
5	57	100.0	36	15	Fibrin polymerizac
6	57	100.0	36	21	Peptide ligand for
7	57	100.0	36	23	Fibrinogen B alpha
8	57	100.0	36	23	Human fibrinogen E
9	57	100.0	36	21	Human pancreatic c
10	57	100.0	36	15	Fibronectin. Homo

11	57	100.0	644	16	AA882244	Human fibrinogen A
12	57	100.0	847	21	AAV82891	Alphab subunit of
13	53	93.0	10	16	AAW11932	Fibrinogen B-beta-
14	44	77.2	17	23	AAE19125	Thrombin peptide.
15	44	77.2	24	23	AAO21112	Anti-angiogenic a1
16	44	77.2	24	23	AAO21116	Anti-angiogenic a1
17	44	77.2	24	23	AAO21117	Anti-angiogenic a1
18	44	77.2	24	23	AAO21118	Anti-angiogenic a1
19	44	77.2	24	23	AAO21119	Anti-angiogenic a1
20	41	71.9	10	19	AAW65536	Biotinyl-fibrin-an
21	38	66.7	24	23	AAO21113	Anti-angiogenic a1
22	38	66.7	24	23	AAO21114	Anti-angiogenic a1
23	38	66.7	24	23	AAO21115	Anti-angiogenic a1
24	38	66.7	24	23	AAO21120	Anti-angiogenic a1
25	38	66.7	24	23	AAO21121	Anti-angiogenic a1
26	38	66.7	29	16	AAW74219	Human ageing marke
27	38	66.7	29	18	AAW14475	Human senility mar
28	38	66.7	29	20	AAW06995	Senscence marker
29	37	64.9	140	22	ABG04700	Novel human diagno
30	37	64.9	323	23	AAU93178	Arabidopsis transc
31	37	64.9	325	22	ABG20112	Novel human diagno
32	37	64.9	336	18	AAW23397	Twik-1 potassium c
33	37	64.9	336	21	AAW79673	Human potassium ch
34	36	63.2	7	8	AAW71315	Sequence of fibrin
35	36	63.2	7	11	AAW06526	Peptide antigenic
36	36	63.2	8	15	AAW65794	Fibrin-specific ep
37	36	63.2	12	8	AAW71099	Functional site re
38	36	63.2	24	19	AAW64264	Murine 34-, 40 and
39	36	63.2	50	22	ABG28568	Novel human diagno
40	36	63.2	132	22	ABG26016	Novel human diagno
41	35	61.4	73	22	ABG26014	Novel human diagno
42	35	61.4	74	22	ABG26011	Novel human diagno
43	35	61.4	107	23	ABP32045	Human RNA polymera
44	35	61.4	111	27	AAU55722	Propionibacterium
45	35	61.4	214	21	AAV99923	Peptide encoded by

ALIGNMENTS

RESULT 1
ABW76978
ID ABW76978 standard; peptide; 11 AA.
XX
AC ABW76978;
XX
DT 22-JUL-2002 (first entry)
XX
DE Residues 36-46 of human fibrinogen alpha chain precursor.
XX
KW Anti-arthritic; anti-inflammatory; fibrin; rheumatoid polyarthritis;
KW human, fibrinogen alpha chain.
XX
OS Homo sapiens.
XX
PN FR2795735-A1.
XX
PD 05-JAN-2001.
XX
PF 01-JUL-1999; 99FR-0008470.
XX
PR 01-JUL-1999; 99FR-0008470.
XX
PA (UYTO-) UNIV TOULOUSE SABATIER PAUL.
XX
PI Setre G, Sebbag M;
XX WPI; 2001-114394/13.
DR
XX New citrulline-containing polypeptide from fibrin, useful for diagnosis
PT and treatment of rheumatoid polyarthritis
XX
PS Example 1; Page 11; 23pp; French.

XX The present invention relates to a citrulline (Cit) containing
 CC polypeptide derived from all or part of the alpha- or beta-chains of
 CC fibrin by substitution of at least one arginine residue by Cit. The Cit
 CC containing polypeptides can be used for in vitro diagnosis of rheumatoid
 CC polyarthritis (RP), by detecting disease-specific autoantibodies, and
 CC therapeutically for neutralising the RP-associated autoimmune response.
 CC The present sequence is a fragment (residues 36-46) of the human
 CC fibrinogen alpha chain precursor, which was used in an example from the
 CC invention.
 XX
 SQ Sequence 11 AA;
 QY
 Db 1 GPRVERHOSA 11
 1 GPRVERHOSA 11
 Query Match 100.0%; Score 57; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 2
 AAMS0593
 ID AAMS0593 standard; peptide; 12 AA.
 AC AAMS0593;
 XX
 DT 16-JUL-1998 (first entry)
 XX
 DE GPIIb/IIIa receptor ligand with technetium-99m binding moiety.
 XX
 KW Technetium-99m label; thrombus imaging; GPIIb/IIIa receptor; ligand;
 XX binding moiety; branched peptide.
 OS Synthetic.
 XX
 FT Key Location/Qualifiers
 FT Modified-site 12
 FT /note= "Side chain of Lys is linked to an identical
 peptide chain to form a branched peptide"
 XX
 PD US5736122-A
 XX
 PD 07-APR-1998
 XX
 PF 07-JUN-1995; 95US-0482880.
 XX
 PR 07-JUN-1995; 95US-0482880.
 PR 08-FEB-1991; 91US-0653012.
 PR 27-NOV-1991; 91US-0807062.
 PR 21-MAY-1992; 92US-0886052.
 PR 22-JUN-1994; 94US-0264176.
 PR 11-JUL-1994; 94US-0273274.
 PR 07-JUN-1995; 95US-0480551.
 XX
 PA (DIAT-) DIATIDE INC.
 XX
 PI Dean RT, Lister-James J;
 XX
 DR WPI, 1998-239148/21.
 XX
 PT Reagent useful for preparing thrombus imaging agent - comprises
 PT peptide covalently linked to technetium binding moiety which is
 PT technetium labelled and binds to thrombus component
 XX
 PS Example 2; Columns 11-12; 18pp; English.
 XX
 CC The invention relates to a reagent for preparing a thrombus imaging
 CC agent. It comprises: (a) a specific binding peptide (BP) having a
 CC sequence of 4-100 amino acids; and (b) a technetium-99m binding moiety
 CC (TBM) covalently linked to the peptide which binds to a component of a
 CC thrombus. TBM forms an electrically neutral complex with technetium-99m.

CC The small size of the peptide component of the reagent enhances blood
 CC and background tissue clearance and it is easy to prepare. This
 CC sequence represents a GPIIb/IIIa receptor binding peptide covalently
 CC linked to a technetium-99m binding moiety.
 XX
 SQ Sequence 12 AA;
 QY
 Db 1 GPRVERHOSA 11
 1 GPRVERHOSA 11
 Query Match 100.0%; Score 57; DB 19; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 3
 AAB13511
 ID AAB13511 standard; peptide; 13 AA.
 AC AAB13511;
 XX
 DT 02-NOV-2000 (first entry)
 XX
 DE Fibrin derived peptide.
 XX
 KW Fibrin derivative; diagnostic agent; therapeutic agent.
 XX
 OS Unidentified.
 XX
 FT Key Location/Qualifiers
 FT Cross-links 12
 FT /note= "this peptide is linked to a second copy of this
 peptide by a disulphide bond to form a dimer"
 XX
 XX
 PN US6077939-A.
 XX
 PD 20-JUN-2000.
 XX
 PF 04-AUG-1997; 97US-0905310.
 XX
 PR 04-AUG-1997; 97US-0905310.
 XX
 PA (ORTH) ORTHOMCNEIL PHARM INC.
 XX
 PI Wei Z, Ghosh-Dastidar P, Menon-Rudolph S;
 XX
 DR WPI, 2000-450981/39.
 XX
 PT Covalently binding a water-soluble polymer to the N-terminal
 PT alpha-carbon atom of a polypeptide for producing therapeutic and
 PT diagnostic agents, by contacting the transaminated polypeptide with the
 PT polymer to form a hydrazone bond
 XX
 PS Example 7; Column 14; 21pp; English.
 XX
 CC The present sequence is a peptide derivative of fibrin. It was used as an
 CC example of the method of the invention, which involves the production of
 CC compositions comprising a polypeptide with a water soluble polymer
 CC covalently bound to the N-terminal alpha carbon by a hydrazone or an
 CC oxime (or the reduced version of each) bond. This is useful as previous
 CC methods were more time consuming and labour-intensive, as well as being
 CC less precise. The composition can be used to produce diagnostic and
 CC therapeutic agents.
 XX
 SQ Sequence 13 AA;
 QY
 Db 1 GPRVERHOSA 11
 1 GPRVERHOSA 11
 Query Match 100.0%; Score 57; DB 21; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GPRVERHOSA 11

RESULT 4

AA69318 ID AAR69318 standard; peptide; 15 AA.

AC AAR69318;

DT 25-JUN-1995 (first entry)

DE Gp IIb/IIIa receptor ligand used in scintigraphic imaging of thrombi.

XX Scintigraphy; thrombus; thrombi; imaging; specific binding;

KM Technetium-99m; radiolabelled; Gp IIb/IIIa receptor ligand.

XX Synthetic.

OS Key Location/Qualifiers

FT Modified-site 12 /note= "the omega-amino of this Lys is substd. by

FT Modified-site 13 /note= "S-acetamidomethyl-Cys"

FT Modified-site 15 /note= "S-acetamidomethyl-Cys-amide"

PN WO9323085-A.

PD 25-NOV-1993.

PF 21-MAY-1993; 93WO-US04794.

PR 21-MAY-1992; 92US-0886752.

XX (DIAT-) DIATECH INC.

PI Dean RT, Lister-James J;

DR WPI; 1993-366229/48.

PT Reagent for scintigraphic imaging of thrombi with 99m technetium
PT - comprises synthetic peptide which binds to thrombus, covalently
PT coupled to metal binding gp.; rapidly cleared from blood and
PT tissue

PS Claim 19; Page 42; 61pp; English.

XX The invention relates to reagents for scintigraphic imaging of a
CC thrombus in-vivo, comprising (A) a specific binding compound capable of
CC binding to at least one component of a thrombus, covalently linked
CC to (B) a technetium-99m-binding moiety. Specific peptides
CC constituting the reagents are claimed as new. The present peptide is
CC one such peptide, in which the Cys(Acm)-Gly-Cys(Acm) moiety is the
CC 99m-Tc binding moiety and the residue constitutes the thrombus-
CC binding component.

XX Sequence 15 AA;

Query Match 100.0%; Score 57; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRVERHOSA 11

Db 1 GPRVERHOSA 11

RESULT 5

AA95518

ID AAY95518 standard; peptide; 15 AA.

AC AAY95518;

XX 10-OCT-2000 (first entry)

XX .Fibrin polymerization site ligand.

XX Thrombus; imaging; radioimaging; thrombosis; thromboembolism;

KM embolism; diagnosis; technetium-99m; fibrin ligand.

XX Synthetic.

OS Key Location/Qualifiers

FT Peptide 1.11 /note= "2 copies of this peptide are covalently
FT attached to the Lys residue at position 12"

FT Modified-site 13 /note= "Cys(Acm)"

FT Modified-site 15 /note= "Cys(Acm)"

FT Modified-site 15 /note= "C-terminal amide"

PN US6083481-A.

PD 04-JUL-2000.

PF 27-AUG-1998; 98US-0141127.

PR 21-MAY-1992; 92US-0886752.

PR 21-MAY-1993; 93WO-US04794.

PR 05-JAN-1995; 95US-0335832.

XX (DIAT-) DIATIDE INC.

PI Lister-James J, Dean RT;

DR WPI; 2000-498061/44.

PT Composition comprises technetium-99m and polyamide reagent which binds
PT to thrombi, useful as scintigraphic imaging agent for imaging sites of
PT thrombus formation in vivo

PS Disclosure; Column 10; 27pp; English.

XX The present sequence is that of a ligand for the fibrin
CC polymerization site. The invention relates to radiolabeled
CC reagents that are scintigraphic imaging agents for imaging sites of
CC thrombus formation in vivo. The reagents each comprise a specific
CC binding compound, such as the present peptide, that is capable of
CC binding to at least 1 component of a thrombus, and which is
CC covalently linked to a radiolabel-binding moiety. A method for
CC using such a reagent labeled with technetium-99m to image a
CC thrombus site in a mammalian body is claimed.

XX Sequence 15 AA;

Query Match 100.0%; Score 57; DB 21; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRVERHOSA 11

Db 1 GPRVERHOSA 11

RESULT 6

AA54925

ID AAY54925 standard; peptide; 23 AA.

AC AAY54925;

DT 15-FEB-2000 (first entry)

XX Peptide ligand for fibrin polymerization site.

XX Thrombus imaging; fibrin polymerisation site; technetium-99m; Tc-99m;
 KW GPIIb/IIIa receptor; cyclic peptide ligand.
 XX Synthetic.
 OS
 PN US5968476-A.
 XX
 PD 19-OCT-1999.
 XX
 PF 07-JUN-1995; 95US-0484773.
 XX
 PR 11-JUL-1994; 94US-0273274.
 PR 21-MAY-1992; 92US-0886052.
 XX
 PA (DIAT-) DIATIDE INC.
 XX
 PI Dean RT, Lister-James J;
 DR WPI; 2000-02173/02.
 XX
 PT A complex used for thrombus imaging comprises technetium-99m complexed
 PT with a peptide ligand for GPIIb/IIIa receptor
 XX
 PS Claim 8; Column 32; 18pp; English.
 XX
 CC This sequence represents a peptide ligand for the fibrin polymerisation
 CC site. The invention relates to a complex (A) for thrombus imaging
 CC comprising technetium-99m (Tc-99m) complexed with a reagent comprising a
 CC peptide (P) with 4 to 100 amino acids sequence and a Tc-99m binding
 CC moiety covalently bound to (P). (P) is selected from a linear peptide
 CC ligand for a GPIIb/IIIa receptor not comprising the amino acid sequence
 CC (arginine-glycine-aspartate), a peptide ligand for a polymerisation
 CC site of fibrin, and a cyclic peptide ligand for the GPIIb/IIIa receptor.
 CC The thrombus imaging reagents provided by the present invention can be
 CC used for visualising thrombi in a mammalian body when Tc-99m is labelled.
 XX
 SQ Sequence 23 AA;
 Query Match 100.0%; Score 57; DB 21; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.00032;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRVERHOSA 11
 DB 1 GPRVERHOSA 11
 RESULT 7
 AAO21122
 ID AAO21122 standard; Protein; 78 AA.
 XX
 AC AAO21122;
 XX
 DT 19-JUL-2002 (first entry)
 XX
 DE Fibrinogen E alpha-chain protein sequence.
 XX
 KW Cytosratic; antitumour; ophthalmological; antiarthritic; antirheumatic;
 KW antipruritic; antidiabetic; anti-angiogenic; alpha1-24 peptide; tumour;
 KW fibrinogen; cancer; angiogenesis; chemotherapeutic agent; psoriasis;
 KW neovascular glaucoma; rheumatoid arthritis; diabetic retinopathy;
 KW gene therapy.
 XX
 OS Unidentified.
 XX
 PN WO200218440-A1.
 XX
 PD 07-MAR-2002.
 XX
 PF 03-SEP-2001; 2001WO-GB03926.
 XX
 PR 01-SEP-2000; 2000GB-0021475.

PR 09-NOV-2000; 2000GB-0027395.
 PR 27-NOV-2000; 2000US-252896P.
 PR 23-JUL-2001; 2001GB-0017737.
 XX
 XX (BIO-) BIOACTA LTD.
 XX
 PI Staton C, Lewis C, Robinson J;
 XX
 DR WPI; 2002-339656/37.
 DR N-PSDB; AAK99966.
 XX
 PT Novel polypeptide comprising anti-angiogenic alpha 1-24 peptide
 PT sequence derived from fibrinogen, useful for inhibiting angiogenesis in
 PT conditions such as cancer, neovascular glaucoma, psoriasis, rheumatoid
 PT arthritis
 XX
 PS Disclosure; Fig 1; 49pp; English.
 XX
 CC The invention relates to a polypeptide comprising an anti-angiogenic
 CC alpha 1-24 peptide sequence derived from fibrinogen. The peptide
 CC comprising ADSGSDPLAGSGVGRVERH (alpha 1-24 peptide) is useful for
 CC manufacturing a medicament for treating cancer. The peptide, its encoding
 CC DNA, a pharmaceutical composition and vector of the invention are useful
 CC for treating an animal which would benefit from inhibition of
 CC angiogenesis, where the therapeutic agents are administered to the animal
 CC and the effects of the agent on the inhibition of angiogenesis is
 CC monitored. Polypeptides useful for treatment are conjugated, associated
 CC or crosslinked to a chemotherapeutic agent. The method is preferably
 CC carried out for inhibiting tumour angiogenesis in tumours. The peptide,
 CC its encoding DNA, a pharmaceutical composition and vector of the
 CC invention are useful for inhibiting angiogenesis in conditions of
 CC neovascular glaucoma, rheumatoid arthritis, psoriasis, or diabetic
 CC retinopathy. The DNA of the alpha 1-24 peptide can be used in gene
 CC therapy. This sequence represents a fibrinogen E alpha-chain protein
 CC sequence of the invention.
 XX
 SQ Sequence 78 AA;
 Query Match 100.0%; Score 57; DB 23; Length 78;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRVERHOSA 11
 DB 17 GPRVERHOSA 27
 RESULT 8
 AAO14005
 ID AAO14005 standard; protein; 78 AA.
 XX
 AC AAO14005;
 XX
 DT 28-MAY-2002 (first entry)
 XX
 DE Human fibrinogen E-fragment alpha-chain amino acids 1-78.
 XX
 KW Human fibrinogen E-fragment; alpha-chain; anti-angiogenesis;
 KW angiogenesis; blood vessel development; cellular matrix; plasmin;
 KW thrombin; breast carcinoma; cancer; imaging agent;
 KW tumour identification; tumour growth inhibition;
 KW neovascular glaucoma; diabetic retinopathy;
 KW age-related macular degeneration; haemangioma; Kaposi's sarcoma;
 KW ovarian hyperstimulation; obesity; hepatitis; pneumonia;
 KW glomerulonephritis.
 XX
 OS Homo sapiens.
 XX
 PN WO200188129-A1.
 XX
 PD 22-NOV-2001.
 XX
 PF 14-MAY-2001; 2001WO-GB02079.

XX 13-MAY-2000; 2000GB-0011464.
 PR 14-JUN-2000; 2000GB-0014370.
 PR 09-NOV-2000; 2000GB-0027396.
 XX
 PA (UYSH-) UNIV SHEFFIELD.
 XX
 PI Lewis C, Staton C;
 XX
 DR WPI: 2002-062380/08.
 DR N-PSDB; AAK98254.
 XX
 PT Novel isolated nucleic acid molecule which encodes a fibrinogen E
 PT polypeptide which is useful for treating cancer, diabetic retinopathy,
 PT obesity, hepatitis, pneumonia, glomerulonephritis, asthma and
 PT thyroiditis -
 XX
 PS Claim 6; Fig 1; 41pp; English.
 XX
 CC The present sequence represents amino acids 1-78 of the human fibrinogen
 CC E-fragment alpha-chain. The invention comprises DNA sequences encoding
 CC fibrinogen E-fragment polypeptides possessing anti-angiogenesis
 CC properties. Angiogenesis, the development of new blood vessels from an
 CC existing vascular bed, is a multistep process involving the degradation
 CC of components of the cellular matrix, leading to the migration,
 CC proliferation and differentiation of endothelial cells to form tubules
 CC and eventually new vessels. Fibrinogen (the soluble circulating precursor
 CC of fibrin) is a dimeric molecule containing pairs of non-identical chains
 CC (i.e. alpha, beta and gamma chains). The chains are arranged as three
 CC domains, the two outer D-domains and the central E-domain. Fibrinogen can
 CC be digested by either plasmin or thrombin, the fibrin E-fragment produced
 CC by proteolytic cleavage of fibrin stimulates angiogenesis in the
 CC choriocallantoic membrane assay. Further the amount of this protein
 CC present in invasive breast carcinomas positively correlates with the
 CC degree of tumour vascularity. This invention has discovered proteolytic
 CC fragments of fibrinogen that inhibit angiogenesis. The nucleic acids and
 CC proteins of the invention are useful in the manufacture of a medicament
 CC for treating cancer, and for treating a human or animal which would
 CC benefit from inhibition of angiogenesis. The proteins of the invention
 CC are useful to target imaging agents, (e.g. to identify developing tumours
 CC or to monitor the effect of treatment to inhibit tumour growth). The
 CC proteins of the invention are also useful in modulating angiogenesis for
 CC the treatment of: ophthalmological conditions (e.g. neovascular glaucoma,
 CC diabetic retinopathy and age-related macular degeneration); pathological
 CC conditions (e.g. haemangioma, Kaposi's sarcoma, ovarian hyperstimulation,
 CC and obesity); inflammatory and infectious processes (e.g. hepatitis,
 CC pneumonia, and glomerulonephritis).
 CC
 XX
 SQ Sequence 78 AA;
 XX
 Query Match 100.0%; Score 57; DB 23; Length 78;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRVERHQSA 11
 |||||
 DB 17 GPRVERHQSA 27

KW linkage analysis; tissue identification; tissue typing; forensic;
 KW neural; immune system; muscular; reproductive; gastrointestinal;
 KW pulmonary; cardiovascular; renal; proliferative.
 XX
 OS Homo sapiens.
 XX
 PN WO200055320-A1.
 XX
 PD 21-SEP-2000.
 XX
 PF 08-MAR-2000; 2000MO-US05989.
 XX
 PR 12-MAR-1999; 99US-0124270.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM;
 XX
 DR WPI: 2000-579444/54.
 DR N-PSDB; AAC98900.
 XX
 PT New nucleic acid that is a pancreatic cancer antigen for preventing,
 PT treating, or ameliorating a medical condition, particular pancreatic
 PT cancer, or for use in assays for diagnosing a pathological condition -
 XX
 Claim 11; Page 1024-1026; 1379pp; English.
 XX
 CC AAC98773 to AAC99231 encode the human pancreatic cancer associated
 CC proteins, called pancreatic cancer antigens, given in AAB54008 to
 CC AAB54466. The human pancreatic cancer antigens have cytostatic,
 CC neuroprotective, neurotropic, immunomodulatory, relaxant, contraceptive,
 CC gynaecological, cardiant and antiinflammatory activities, and can be used
 CC in gene therapy. The polynucleotide and proteins can be used for
 CC preventing, treating, or ameliorating a medical condition or in assays
 CC for diagnosing a pathological condition or a susceptibility to one in a
 CC subject. Binding partners to the proteins and the activity of the
 CC proteins can be identified. The pancreatic cancer antigens can be used to
 CC detect, treat or prevent pancreatic disorders, especially cancer.
 CC Aponists and antagonists to the antigens can be screened for. The
 CC pancreatic cancer antigen polynucleotides can be used to design nucleic
 CC acid hybridisation probes that can be used in chromosome mapping, linkage
 CC analysis, tissue identification and/or typing and a variety of forensic
 CC and diagnostic methods. The proteins can be used to generate antibodies
 CC which are used to purify, detect and target the polypeptides, including
 CC both in vivo and in vitro diagnostic and therapeutic methods. The
 CC proteins can be used to treat or prevent neural, immune system, muscular,
 CC reproductive, gastrointestinal, pulmonary, cardiovascular, renal or
 CC CC proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent
 CC sequences used in the exemplification of the present invention.
 XX
 SQ Sequence 360 AA;
 XX
 Query Match 100.0%; Score 57; DB 21; Length 360;
 Best Local Similarity 100.0%; Pred. No. 0.0065;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRVERHQSA 11
 |||||
 DB 57 GPRVERHQSA 67

RESULT 9
 AAB54135
 ID AAB54135 standard; Protein; 360 AA.
 XX
 AC AAB54135;
 XX
 DT 09-MAR-2001 (first entry)
 XX
 DE Human pancreatic cancer antigen protein sequence SEQ ID NO:587.
 XX
 KW Human; pancreas; pancreatic cancer; pancreatic cancer antigen;
 KW detection; diagnosis; identification; cytostatic; neuroprotective;
 KW neurotropic; immunomodulatory; relaxant; contraceptive; gynaecological;
 KW antiinflammatory; cardiant; gene therapy; chromosome mapping;

RESULT 10
 AAR60020
 ID AAR60020 standard; Protein; 643 AA.
 XX
 AC AAR60020;
 XX
 DT 23-FEB-1995 (first entry)
 XX
 DE Fibronectin.
 XX
 KW Tissue binding; tissue sealing; wound healing; vulnery;
 KW tissue-binding domain; TBD; crosslinking domain; fibronectin;

```

PN      WO9523868-A1.
XX
PD      08-SEP-1995.
XX
PF      01-MAR-1995;      95WO-US02648.
XX
PR      03-MAR-1994;      94US-0206176.
XX
PA      (PHAR-) PHARM PROTEINS LTD.
PA      (ZYMO ) ZYMOGENETICS INC.
XX
PI      Dairyple MA, Foster DC, Garner I, Prunkard DE;
XX      WPI; 1995-320582/41.
XX      N-PSDB; AAT03853.
XX
PT      Production of fibrinogen in transgenic mammals - by introducing DNA
PT      segments into the germ line of a non-human mammal and collecting
XX      milk from female progeny.
PS      Disclosure; Page 42-44; 99pp; English.
XX
CC      Human fibrinogen A-alpha chain may be produced recombinantly,
CC      preferably by sheep beta-lactoglobulin signal peptide fusion
CC      protein gene expression in non-human transgenic animal milk.
CC      preferably of a sheep, pig, goat or cattle. Co-expression with the
CC      fibrinogen B-beta chain (see AAR82243) and the gamma chain (see
CC      AAR82245) results in the production of active fibrinogen, which is
CC      useful in human and veterinary medicine, e.g. in the formulation of
CC      surgical adhesives, which also consist of Factor XIII, and as a
CC      coating surface for polymeric articles, such as synthetic vascular
XX      grafts.
SQ      Sequence      644 AA;

Query Match      100.0%; Score 57; DB 16; Length 644;
Best Local Similarity 100.0%; Pred. No. 0.012; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0;

OY      1 GPRVERHOSA 11
      |||||
      36 GPRVERHOSA 46

Db

RESULT 12
AAy82891
ID      AAY82891 standard; Protein; 847 AA.
XX
AC      AAY82891;
XX
DT      19-JUN-2000 (first entry)
XX
DE      AlphaE subunit of human fibrinogen.
XX
KW      Fibrinogen; blood; blood clotting; Plasminogen activator;
KW      urokinase; streptokinase; alpha subunit; beta subunit; gamma subunit;
KW      myocardial infarction; reperfusion; atherogenesis; alphaEC; alphaECX;
XX      human; trauma; wound repair; angiogenesis; cancer.
OS      Homo sapiens.
XX
PN      WO200009562-A1.
XX
PD      24-FEB-2000.
XX
PF      12-AUG-1999;      99WO-US18412.
XX
PR      12-AUG-1998;      98US-0096210.
XX
PA      (NYBL-) NEW YORK BLOOD CENT INC.
XX
PI      Grieninger G, Applegate D, Stoike-steben L;
XX

```

DR WPI; 2000-205983/18.
 DR N-PSDB; AAZ93039.
 XX
 PT New fragments of human fibrinogen, useful for treating conditions
 XX associated with fibrinogen metabolism -
 PS Disclosure; Page 59-62; 66pp; English.
 XX
 CC Fibrinogen has a complex structure comprising two copies of alpha,
 CC beta and gamma subunits in a heavily disulfide bonded hexamer. Until
 CC recently it was thought that the alpha subunits lacked a globular
 CC C-terminal domain which was present on the beta and gamma subunits.
 CC However, an additional exon (exon VI) downstream of the alpha subunit
 CC gene and additional splicing leads to the use of this extra sequence
 CC to elongate the alpha chain by 35* (236 amino acids), providing the
 CC alpha subunit with a globular C-terminal domain. Isolated fragments
 CC of human fibrinogen termed 'alphaECX cleavage fragments' derived
 CC from this globular C-terminal domain can be administered
 CC therapeutically to treat mammals (especially humans) suffering from
 CC conditions associated with fibrinogen metabolism e.g. trauma
 CC requiring wound repair, angiogenesis and cancer. They are useful
 CC diagnostically to detect a fibrinogen alphaECX domain in vivo or in
 CC vitro; the presence of alphaECX cleavage fragments indicates
 CC proteolytic degradation of fibrinogen-420 (the subclass of human
 CC fibrinogen containing the alphaEC domain) and can be used to
 CC determine a fibrinolytic state or atherogenesis. Such diagnosis is
 CC useful e.g. to regulate the amount of 'plasminogen activator'
 CC (i.e. compounds used to induce/enhance thrombolysis such as
 CC urokinase, plasminogen activator and streptokinase) given,
 CC especially useful since these compounds require stringent
 CC control and can cause bleeding complications in patients. The
 CC diagnostic method can also be used to diagnose a myocardial
 CC infarction or monitor reperfusion in a mammal with a myocardial
 CC infarction. This sequence is the Alpha subunit of fibrinogen. The
 CC C-terminal 236 amino acids comprise the alphaECX domain.
 XX
 SQ Sequence 847 AA;
 Query Match 100.0%; Score 57; DB 21; Length 847;
 Best Local Similarity 100.0%; Pred. No. 0.017;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRVERHQA 11
 |||||
 DB 17 GPRVERHQA 27
 RESULT 13
 AAM1932
 ID AAM1932 standard; peptide; 10 AA.
 XX
 AC AAM1932;
 XX
 DT 02-APR-1997 (first entry)
 XX
 DE Fibrinogen B-beta-chain residues 15-24.
 XX
 KM Monoclonal; antibody; human; soluble; fibrin; fibrinogen;
 KM urea-treated; des-AAAB; B-beta-chain; immunoassay; diagnosis;
 KM disseminated intravascular coagulation.
 XX
 OS Homo sapiens.
 OS
 PN WO9512617-A1.
 PD 11-MAY-1995.
 XX
 PF 01-NOV-1994; 94WO-JP01844.
 XX
 PR 02-NOV-1993; 93JP-0297325.
 XX
 PA (IATR) IATRON LAB INC.
 XX

PI Inuzuka K, Ito Y, Kohno I, Soe G;
 XX
 DR WPI; 1995-206667/27.
 XX
 PT Monoclonal antibody reactive with soluble human fibrin - but not
 PT with fibrinogen, is useful for fibrin immunoassay in plasma
 PT specimens
 XX
 PS Example 3; Page 15; 32pp; Japanese.
 XX
 CC A novel monoclonal antibody (MAb) reacts with human soluble fibrin,
 CC but not with human fibrinogen. Specifically when the MAb reacts
 CC with urea-treated des-AAAB fibrin the reaction is not inhibited by
 CC peptides corresponding to fibrinogen A-alpha-chain residues 17-26
 CC (AAM1931), B-beta-chain residues 15-24 (AAM1932) or gamma-chain
 CC residues 312-324 (AAM1933). The MAb is useful in immunoassays for
 CC soluble fibrin in plasma samples (e.g. by sandwich immunoassay),
 CC particularly for the diagnosis of pathological conditions such as
 CC disseminated intravascular coagulation.
 XX
 SQ Sequence 10 AA;
 Query Match 93.0%; Score 53; DB 16; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00079;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRVERHQA 10
 |||||
 DB 1 GPRVERHQA 10
 RESULT 14
 AAE19125
 ID AAE19125 standard; peptide; 17 AA.
 XX
 AC AAE19125;
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DE Thrombin peptide.
 XX
 KM Luciferase; enzyme; protease; cell growth; apoptosis; therapeutic;
 KM cell death; thrombin.
 XX
 OS Unidentified.
 XX
 PN WO200206458-A2.
 PD 24-JAN-2002.
 XX
 PF 17-JUL-2001; 2001WO-US22478.
 XX
 PR 19-JUL-2000; 2000US-0619047.
 XX
 PA (CHEM-) CHEMICON INT INC.
 XX
 PI Leng J;
 XX
 DR WPI; 2002-195809/25.
 XX
 PT New purified luciferase polypeptide, useful for identifying protease
 PT activity modulators, comprises recognition site cleavable by protease,
 PT where cleavage of polypeptide results in decreased luciferase activity
 PT
 XX
 PS Claim 63; Page 24; 56pp; English.
 XX
 CC The invention relates to a purified polypeptide having luciferase
 CC activity and a recognition site specifically cleavable by a protease,
 CC where cleavage results in a decrease in luciferase activity. The
 CC polypeptide comprises a localisation sequence which is linked to the
 CC luciferase polypeptide by the cleavable recognition sequence. The
 CC polypeptide is useful for identifying a protease (Caspase-3) activity

CC modulator, an inhibitor of apoptosis and for detecting luciferase
 CC activity in a sample. The polypeptide is used for characterizing and
 CC identifying cellular processes associated with metabolism, cell growth
 CC and cell death e.g. apoptosis and for measuring protease activity. The
 CC protease measurement methods are useful for characterizing, identifying
 CC cellular biochemical pathways as well as identifying diagnostic and
 CC agents for modulating diseases or disorders associated with
 CC biochemical pathways. The polypeptide is also useful as a substrate to
 CC study agents or conditions that cleave the recognition site and for
 CC determining amount of protease in a sample and for monitoring the
 CC activity of protease inside a cell that expresses a recombinant
 CC luciferase. The present sequence is thrombin peptide used in the
 CC invention.

SO Sequence 17 AA;

Query Match 77.2%; Score 44; DB 23; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.083;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPRVERH 8
 Db 10 GPRVERH 17

RESULT 15

ID AAO21112
 XX AAO21112 standard; Peptide; 24 AA.

AC AAO21112;

DT 19-JUL-2002 (first entry)

DE Anti-angiogenic alpha 1-24 peptide #2.

XX Cytostatic; antitumor; ophthalmological; antiarthritic; antirheumatic;
 KW antipsoriatic; antidiabetic; anti-angiogenic; alpha1-24 peptide; tumour;
 KW fibrogen; cancer; angiogenesis; chemotherapeutic agent; psoriasis;
 KW neovascular glaucoma; rheumatoid arthritis; diabetic retinopathy;
 KW gene therapy.

OS Unidentified.

FN WO200218440-A1.

PD 07-MAR-2002.

PF 03-SEP-2001; 2001WO-GB03926.

PR 01-SEP-2000; 2000GB-0021475.

PR 09-NOV-2000; 2000GB-0027395.

PR 27-NOV-2000; 2000US-252886P.

PR 23-JUL-2001; 2001GB-0017737.

PA (BIOA-) BIOACTA LTD.

PI Staton C, Lewis C, Robinson J;

DR WPI; 2002-339656/37.

XX Novel polypeptide comprising anti-angiogenic alpha 1-24 peptide

PT sequence derived from fibrinogen, useful for inhibiting angiogenesis in

PT conditions such as cancer, neovascular glaucoma, psoriasis, rheumatoid

XX arthritis

PS Claim 2; Page 23; 49p; English.

CC angiogenesis, where the therapeutic agents are administered to the animal
 CC and the effects of the agent on the inhibition of angiogenesis is
 CC monitored. Polypeptides useful for treatment are conjugated, associated
 CC or crosslinked to a chemotherapeutic agent. The method is preferably
 CC carried out for inhibiting tumour angiogenesis in tumours. The peptide,
 CC its encoding DNA, a pharmaceutical composition and vector of the
 CC invention are useful for inhibiting angiogenesis in conditions of the
 CC neovascular glaucoma, rheumatoid arthritis, psoriasis, or diabetic
 CC retinopathy. The DNA of the alpha 1-24 peptide can be used in gene
 CC therapy. This sequence represents an anti-angiogenic alpha 1-24 peptide
 CC of the invention.

SO Sequence 24 AA;

Query Match 77.2%; Score 44; DB 23; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPRVERH 8
 Db 17 GPRVERH 24

Search completed: June 27, 2003, 17:16:47
 Job time : 34.55 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 17:18:12 ; Search time 34.1 Seconds
(without alignments)
35.370 Million cell updates/sec

Title: US-10-019-439-1
Sequence: 1 GPRVRRHOSA 11

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 424699 seqs, 109646833 residues

Total number of hits satisfying chosen parameters: 424699

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep:*
4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep:*
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10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep:*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	360	US-09-925-297-587	Sequence 587, App
2	57	100.0	620	US-09-931-009A-1	Sequence 1, Appl
3	57	100.0	644	US-09-919-039-121	Sequence 121, App
4	57	100.0	847	US-10-112-527-4	Sequence 4, Appl
5	45	78.9	9	US-09-953-657-5	GENERAL INFORMA
6	44	77.2	17	US-10-057-505-11	Sequence 11, Appl
7	41	71.9	10	US-09-765-614B-10	Sequence 10, Appl
8	41	71.9	10	US-09-925-715-7	Sequence 7, Appl
9	37	64.9	336	US-10-205-823-190	Sequence 190, App
10	37	64.9	336	US-09-939-484-2	Sequence 2, Appl
11	37	64.9	336	US-09-939-483-2	Sequence 2, Appl
12	36	63.2	581	US-10-025-222A-22	Sequence 22, Appl
13	34	59.6	45	US-10-062-831-106	Sequence 106, App
14	34	59.6	90	US-09-864-761-46461	Sequence 46461, A
15	34	59.6	208	US-10-063-831-79	Sequence 79, Appl
16	34	59.6	347	US-09-815-242-11695	Sequence 11695, A
17	34	59.6	467	US-10-062-831-50	Sequence 50, App
18	34	59.6	510	US-09-925-302-486	Sequence 486, App
19	34	59.6	712	US-09-925-302-678	Sequence 678, App

20	34	59.6	3472	9	US-10-027-806-4	Sequence 4, Appl
21	34	59.6	3472	9	US-10-034-623-4	Sequence 4, Appl
22	34	59.6	3472	9	US-10-027-801-4	Sequence 4, Appl
23	34	59.6	3571	9	US-10-150-821-2	Sequence 2, Appl
24	34	59.6	3571	10	US-09-911-842-2	Sequence 2, Appl
25	33	57.9	59	9	US-09-948-783-201	Sequence 201, App
26	33	57.9	60	9	US-09-992-877-1201	Sequence 201, App
27	33	57.9	145	10	US-09-925-300-1100	Sequence 1300, App
28	33	57.9	532	9	US-09-911-514-2	Sequence 2, Appl
29	33	57.9	532	10	US-09-911-514-2	Sequence 2, Appl
30	33	57.9	3594	9	US-10-150-821-4	Sequence 4, Appl
31	33	57.9	3594	10	US-09-911-842-4	Sequence 4, Appl
32	32	56.1	116	9	US-10-023-282-1065	Sequence 1065, App
33	32	56.1	140	10	US-09-764-877-1654	Sequence 1654, App
34	32	56.1	193	10	US-09-764-898-214	Sequence 214, App
35	32	56.1	219	9	US-09-975-119-415	Sequence 415, App
36	32	56.1	368	10	US-09-815-242-11651	Sequence 11651, A
37	32	56.1	375	10	US-09-815-242-10928	Sequence 10928, A
38	32	56.1	417	9	US-09-823-187-64	Sequence 64, Appl
39	32	56.1	508	9	US-09-895-298-92	Sequence 92, Appl
40	32	56.1	541	9	US-10-011-548-28	Sequence 28, Appl
41	32	56.1	541	10	US-09-981-421-4	Sequence 4, Appl
42	32	56.1	541	12	US-10-157-447-2	Sequence 2, Appl
43	32	56.1	545	10	US-09-815-242-10275	Sequence 10275, A
44	32	56.1	549	10	US-09-801-368-358	Sequence 358, App
45	31	54.4	90	10	US-09-864-761-33556	Sequence 33556, A

ALIGNMENTS

RESULT 1
US-09-925-297-587
Sequence 587, Application US/09925297
Patent No. US20020081659A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 928
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 587
LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (15)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (315)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (326)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (337)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (339)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
Query Match 100.0%; Score 57; DB 10; Length 360;

Best Local Similarity 100.0%; Pred. No. 0.009;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRVRRHQA 11
Db 57 GPRVRRHQA 67

RESULT 2

US-09-931-009A-1
; Sequence 1, Application US/09931009A
; Publication No. US20030109431A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Theresa H.
; TITLE OF INVENTION: PRO-INFLAMMATORY FIBRINOPEPTIDE
; FILE REFERENCE: US 1257/01 (VA)
; CURRENT APPLICATION NUMBER: US/09/931,009A
; CURRENT FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 620
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-931-009A-1

Query Match 100.0%; Score 57; DB 9; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRVRRHQA 11
Db 17 GPRVRRHQA 27

RESULT 3

US-09-919-039-121
; Sequence 121, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 121
; LENGTH: 644
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 280276CD1
US-09-919-039-121

Query Match 100.0%; Score 57; DB 9; Length 644;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRVRRHQA 11
Db 36 GPRVRRHQA 46

RESULT 4

US-10-112-527-4
; Sequence 4, Application US/10112527
; Patent No. US20020168722A1
; GENERAL INFORMATION:
; APPLICANT: Grieninger, Gerd

APPLICANT: Applegate, Dianne

APPLICANT: Stoike-Steber, Lara

FILE REFERENCE: No. US20020168722A1 Cleaved Fragments of Fibrinogen

FILE REFERENCE: Docket 454-24 CON

CURRENT APPLICATION NUMBER: US/10/112,527

CURRENT FILING DATE: 2002-03-29

PRIOR APPLICATION NUMBER: US 09/373,157

PRIOR FILING DATE: 1999-08-12

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PatentIn version 3.1

SEQ ID NO 4

LENGTH: 847

TYPE: PRT

ORGANISM: Homo sapiens

US-10-112-527-4

Query Match 100.0%; Score 57; DB 9; Length 847;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRVRRHQA 11
Db 17 GPRVRRHQA 27

RESULT 5

US-09-953-657-5
; GENERAL INFORMATION:
; APPLICANT: Bueltner, Joseph A.
; Dadd, Christopher A.
; Baumbach, George A.
; Hammond, David J.
; TITLE OF INVENTION: Fibrinogen Binding Peptides
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 800 Dwight Way
; P. O. Box 1986
; CITY: Berkeley
; STATE: California
; COUNTRY: USA
; ZIP: 94701-1986
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb Storage
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: Wordperfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/953,657
; FILING DATE: 17-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/595,718
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Gbblin, James A.
; REGISTRATION NUMBER: 25772
; REFERENCE/DOCKET NUMBER: MSB-7233
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510)705-7910
; TELEFAX: (510)705-7904
; JOURNAL: Thromb. Haemost.
; VOLUME: 63
; ISSUE: 3
; PAGES: 439-444
; DATE: 28-JUN-1990
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-953-657-5

Query Match 78.9%; Score 45; DB 10; Length 9;
Best Local Similarity 88.9%; Pred. No. 3.8e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRVERHQ 9
Db 1 GPRVERHK 9

RESULT 6

US-10-057-505-11
; Sequence 11, Application US/10057505
; Patent No. US20020164674A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: AURORA BIOSCIENCES CORPORATION
; APPLICANT: TS'EN, Roger
; APPLICANT: HEIM, Roger
; APPLICANT: CUBITT, Andrew
; TITLE OF INVENTION: TANDEM FLUORESCENT PROTEIN CONSTRUCTS
; FILE REFERENCE: REGEN1260-3
; CURRENT APPLICATION NUMBER: US/10/057,505
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 08/792,553
; PRIOR FILING DATE: 1997-01-31
; PRIOR APPLICATION NUMBER: US 09/396,003
; PRIOR FILING DATE: 1999-09-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Linker moiety
US-10-057-505-11

Query Match 77.2%; Score 44; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRVERH 8
Db 10 GPRVERH 17

RESULT 7

US-09-765-614B-10
; Sequence 10, Application US/09765614B
; Patent No. US20020102215A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to
; TITLE OF INVENTION: diagnostic/therapeutic
; FILE REFERENCE: REF/Klavness/054
; CURRENT APPLICATION NUMBER: US/09/765,614B
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial
; OTHER INFORMATION: Sequence: Biotinylated
; OTHER INFORMATION: fibrin-anti-polymerant peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Biotinylated-Gly
; NAME/KEY: MOD_RES
; LOCATION: (10)
; OTHER INFORMATION: AMIDATION
US-09-765-614B-10

Query Match 71.9%; Score 41; DB 10; Length 10;

Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GPRVERHOS 10
Db 1 GPRPRRHOS 10

RESULT 8

US-09-925-715-7
; Sequence 7, Application US/09925715
; Patent No. US20020102217A1
; GENERAL INFORMATION:
; APPLICANT: Nycomed Imaging AS
; TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
; TITLE OF INVENTION: agents
; FILE REFERENCE: REF/Klavness/206
; CURRENT APPLICATION NUMBER: US/09/925,715
; CURRENT FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Biotinylated
; OTHER INFORMATION: fibrin-antipolymerant peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Biotin-Gly
; NAME/KEY: MOD_RES
; LOCATION: (10)
; OTHER INFORMATION: AMIDATION
US-09-925-715-7

Query Match 71.9%; Score 41; DB 10; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPRVERHOS 10
Db 1 GPRPRRHOS 10

RESULT 9

US-10-205-823-190
; Sequence 190, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarepu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Monsey, Angela M.
; APPLICANT: Gialt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25

;; PRIOR APPLICATION NUMBER: 60/341,746
;; PRIOR FILING DATE: 2001-12-12
;; PRIOR APPLICATION NUMBER: 60/362,158
;; PRIOR FILING DATE: 2002-03-05
;; NUMBER OF SEQ ID NOS: 455
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 190
;; LENGTH: 336
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-205-823-190

Query Match
Best Local Similarity 64.9%; Score 37; DB 9; Length 336;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVERHQSA 11
Db 12 RVERHRSR 20

RESULT 10
US-09-939-484-2
;; Sequence 2, Application US/09939484
;; Patent No. US2002003322A1
;; GENERAL INFORMATION:
;; APPLICANT: Duprat, Fabrice
;; APPLICANT: Lesage, Florian
;; APPLICANT: Fink, Michel
;; APPLICANT: Lazdunski, Michel
;; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
;; FILE REFERENCE: 1201-CIP-DIV-00
;; CURRENT APPLICATION NUMBER: US/09/939,484
;; PRIOR FILING DATE: 2001-08-24
;; PRIOR APPLICATION NUMBER: 09/144,914
;; PRIOR FILING DATE: 1998-09-01
;; PRIOR APPLICATION NUMBER: 08/749,816
;; PRIOR FILING DATE: 1996-11-15
;; PRIOR APPLICATION NUMBER: 60/095,234
;; PRIOR FILING DATE: 1998-08-04
;; PRIOR APPLICATION NUMBER: FR 96/01565
;; PRIOR FILING DATE: 1996-02-08
;; NUMBER OF SEQ ID NOS: 24
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 2
;; LENGTH: 336
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: TWIK-1
US-09-939-484-2

Query Match
Best Local Similarity 64.9%; Score 37; DB 10; Length 336;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVERHQSA 11
Db 12 RVERHRSR 20

RESULT 11
US-09-939-483-2
;; Sequence 2, Application US/09939483
;; Patent No. US20020094558A1
;; GENERAL INFORMATION:
;; APPLICANT: Duprat, Fabrice
;; APPLICANT: Lesage, Florian
;; APPLICANT: Fink, Michel
;; APPLICANT: Lazdunski, Michel
;; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
;; FILE REFERENCE: 1201-CIP-DIV-00
;; CURRENT APPLICATION NUMBER: US/09/939,483
;; PRIOR FILING DATE: 2001-08-24
;; PRIOR APPLICATION NUMBER: 09/144,914
;; PRIOR FILING DATE: 1998-09-01
;; PRIOR APPLICATION NUMBER: 08/749,816
;; PRIOR FILING DATE: 1996-11-15
;; PRIOR APPLICATION NUMBER: 60/095,234
;; PRIOR FILING DATE: 1998-08-04
;; PRIOR APPLICATION NUMBER: FR 96/01565
;; PRIOR FILING DATE: 1996-02-08
;; NUMBER OF SEQ ID NOS: 24
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 2
;; LENGTH: 336
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: TWIK-1
US-09-939-483-2

;; FILE REFERENCE: 1201-CIP-DIV-2-00
;; CURRENT APPLICATION NUMBER: US/09/939,483
;; CURRENT FILING DATE: 2001-08-24
;; PRIOR APPLICATION NUMBER: 09/144,914
;; PRIOR FILING DATE: 1998-09-01
;; PRIOR APPLICATION NUMBER: 08/749,816
;; PRIOR FILING DATE: 1996-11-15
;; PRIOR APPLICATION NUMBER: 60/095,234
;; PRIOR FILING DATE: 1998-08-04
;; PRIOR APPLICATION NUMBER: FR 96/01565
;; NUMBER OF SEQ ID NOS: 24
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 2
;; LENGTH: 336
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: TWIK-1
US-09-939-483-2

Query Match
Best Local Similarity 64.9%; Score 37; DB 10; Length 336;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVERHQSA 11
Db 12 RVERHRSR 20

RESULT 12
US-10-025-222A-22
;; Sequence 22, Application US/10025222A
;; Publication No. US2003000344A1
;; GENERAL INFORMATION:
;; APPLICANT: PELLETIER, JERRY
;; APPLICANT: GROG, PHILIPPE
;; APPLICANT: DUBOW, MICHAEL
;; APPLICANT: STABYLCOCCUS AUREUS GENE AND ITS ENCODED PROTEIN
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS INVOLVING AN ESSENTIAL
;; FILE REFERENCE: 073406-0701
;; CURRENT APPLICATION NUMBER: US/10/025,222A
;; PRIOR FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 60/256,349
;; PRIOR FILING DATE: 2000-12-19
;; NUMBER OF SEQ ID NOS: 41
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 22
;; LENGTH: 581
;; TYPE: PRT
;; ORGANISM: Escherichia coli
US-10-025-222A-22

Query Match
Best Local Similarity 63.2%; Score 36; DB 9; Length 581;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPRVERHQ 9
Db 104 GPRQIERHQ 112

RESULT 13
US-10-062-831-106
;; Sequence 106, Application US/10062831
;; Publication No. US20030105297A1
;; GENERAL INFORMATION:
;; APPLICANT: Steven M. Ruben, et al.
;; TITLE OF INVENTION: 32 Human Secreted Proteins
;; FILE REFERENCE: P2006P1
;; CURRENT APPLICATION NUMBER: US/10/062,831
;; CURRENT FILING DATE: 2002-02-05

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;; PRIOR APPLICATION NUMBER: 09/690,454
;; PRIOR FILING DATE: 1998-11-10
;; PRIOR APPLICATION NUMBER: PCT/US98/10868
;; PRIOR FILING DATE: May 28, 1998
;; PRIOR APPLICATION NUMBER: 60/044,039
;; PRIOR FILING DATE: May 30, 1997
;; PRIOR APPLICATION NUMBER: 60/048,093
;; PRIOR FILING DATE: May 30, 1997
;; PRIOR APPLICATION NUMBER: 60/048,190
;; PRIOR FILING DATE: May 30, 1997
;; PRIOR APPLICATION NUMBER: 60/050,935
;; PRIOR FILING DATE: May 30, 1997
;; PRIOR APPLICATION NUMBER: 60/048,101
;; PRIOR FILING DATE: May 30, 1997
;; PRIOR APPLICATION NUMBER: 60/048,356
;; PRIOR FILING DATE: May 30, 1997
;; PRIOR APPLICATION NUMBER: 60/056,250
;; PRIOR FILING DATE: August 29, 1997
;; PRIOR APPLICATION NUMBER: 60/056,296
;; PRIOR FILING DATE: August 29, 1997
;; PRIOR APPLICATION NUMBER: 60/056,293
;; PRIOR FILING DATE: August 29, 1997
;; NUMBER OF SEQ ID NOS: 229
;; SOFTWARE: Patentin Ver. 2.0
;; SEQ ID NO 106
;; LENGTH: 45
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-062-831-106
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Query Match      59.6%; Score 34; DB 9; Length 45;
Best Local Similarity 55.6%; Pred. No. 17;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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```
QY      2 PRVERHQA 10
Db      17 PRLEAHQN 25
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RESULT 14
US-09-864-761-46461
;; Sequence 46461, Application US/09864761
;; Patent No. US20020048763A1
;; GENERAL INFORMATION:
;; APPLICANT: Penn, Sharon G.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wensheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; FILE REFERENCE: Aecomica-X-1
;; CURRENT APPLICATION NUMBER: US/09/864,761
;; PRIOR FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263,6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
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;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 46461
;; LENGTH: 90
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC002470.5
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.2
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 7.8
;; OTHER INFORMATION: EST_HUMAN HIT: AV655617.1, EVALUE 2.00e-35
;; OTHER INFORMATION: EST_HUMAN HIT: T27867.1, EVALUE 3.00e-24
;; OTHER INFORMATION: SWISSPROT HIT: P05546, EVALUE 3.00e-48
US-09-864-761-46461
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Query Match      59.6%; Score 34; DB 10; Length 90;
Best Local Similarity 70.0%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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```
QY      2 PRVERHQA 11
Db      78 PRVERHQA 87
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RESULT 15
US-10-062-831-79
;; Sequence 79, Application US/10062831
;; Publication No. US20030105297A1
;; GENERAL INFORMATION:
;; APPLICANT: Steven M. Ruben, et al.
;; TITLE OF INVENTION: 32 Human Secreted Proteins
;; FILE REFERENCE: P2006P1
;; CURRENT APPLICATION NUMBER: US/10/062,831
;; PRIOR FILING DATE: 2002-02-05
;; PRIOR APPLICATION NUMBER: 09/690,454
;; PRIOR FILING DATE: 1998-11-10
;; PRIOR APPLICATION NUMBER: PCT/US98/10868
;; PRIOR FILING DATE: May 28, 1998
;; PRIOR APPLICATION NUMBER: 60/044,039
;; PRIOR FILING DATE: May 30, 1997
;; PRIOR APPLICATION NUMBER: 60/048,093
;; PRIOR FILING DATE: May 30, 1997
;; PRIOR APPLICATION NUMBER: 60/048,190
;; PRIOR FILING DATE: May 30, 1997
;; PRIOR APPLICATION NUMBER: 60/050,935
;; PRIOR FILING DATE: May 30, 1997
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: May 30, 1997
;; PRIOR APPLICATION NUMBER: PCT/US01/00671
;; PRIOR FILING DATE: May 30, 1997
;; PRIOR APPLICATION NUMBER: PCT/US01/00672
;; PRIOR FILING DATE: May 30, 1997
;; PRIOR APPLICATION NUMBER: PCT/US01/00673
;; PRIOR FILING DATE: August 29, 1997
;; PRIOR APPLICATION NUMBER: PCT/US01/00674
;; PRIOR FILING DATE: August 29, 1997
;; PRIOR APPLICATION NUMBER: PCT/US01/00675
;; PRIOR FILING DATE: August 29, 1997
;; NUMBER OF SEQ ID NOS: 229
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; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 79
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (148)
; OTHER INFORMATION: "Xaa equals any of the naturally occurring L-amino acids"
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (186)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (208)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-831-79
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Query Match          59.6%; Score 34; DB 9; Length 208;
Best Local Similarity 55.6%; Pred. No. 91;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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QY      2 PRVERHQS 10
        ||::|||:
Db      62 PRLEAHQN 70
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Search completed: June 27, 2003, 17:30:21
Job time : 35.1 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 17:15:46 ; Search time 12.1 Seconds
(without alignments)
26.748 Million cell updates/sec

Title: US-10-019-439-1
Perfect score: 57
Sequence: 1 GPRVHERHQA 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	13	US-08-905-310-12	Sequence 12, Appl
2	57	100.0	643	US-08-551-356-4	Sequence 4, Appl
3	57	100.0	643	PCT-US93-12687-4	Sequence 4, Appl
4	57	100.0	644	US-08-206-176-2	Sequence 2, Appl
5	57	100.0	847	US-09-373-157-4	Sequence 4, Appl
6	53	93.0	10	US-08-448-547-2	Sequence 2, Appl
7	45	78.9	9	US-08-595-718A-5	Sequence 5, Appl
8	44	77.2	17	US-08-792-553-11	Sequence 11, Appl
9	41	71.9	10	US-08-960-054A-10	Sequence 10, Appl
10	41	71.9	10	US-08-958-993A-10	Sequence 10, Appl
11	41	71.9	10	US-08-959-206A-7	Sequence 7, Appl
12	37	64.9	336	US-08-749-816-2	Sequence 2, Appl
13	37	64.9	336	US-09-144-914-2	Sequence 2, Appl
14	36	63.2	7	US-08-762-695-11	Sequence 11, Appl
15	36	63.2	11	US-08-592-500-40	Sequence 40, Appl
16	36	63.2	11	US-08-195-006-40	Sequence 40, Appl
17	36	63.2	11	PCT-US94-07644A-40	Sequence 25, Appl
18	36	63.2	23	US-08-860-808E-25	Sequence 25, Appl
19	36	63.2	24	US-08-978-404B-48	Sequence 48, Appl
20	34	59.6	505	US-09-257-581-5	Sequence 5, Appl
21	34	59.6	505	US-09-257-581-7	Sequence 7, Appl
22	33	57.9	143	US-09-117-853-2	Sequence 27, Appl
23	33	57.9	532	US-08-764-100-27	Sequence 415, Appl
24	33	57.9	219	US-09-199-637A-415	Sequence 20, Appl
25	32	56.1	521	US-08-996-318-20	Sequence 2, Appl
26	32	56.1	541	US-08-604-333-2	Sequence 2, Appl
27	32	56.1	541	US-08-604-333-2	Sequence 2, Appl

28	32	56.1	541	3	US-09-110-618-2	Sequence 2, Appl
29	32	56.1	541	4	US-09-173-151A-28	Sequence 28, Appl
30	32	56.1	732	1	US-08-317-522A-5	Sequence 5, Appl
31	32	56.1	778	1	US-08-439-818A-5	Sequence 5, Appl
32	32	56.1	778	2	US-08-751-965-5	Sequence 5, Appl
33	32	56.1	778	2	US-08-738-975-5	Sequence 5, Appl
34	32	56.1	778	2	US-08-728-626-5	Sequence 5, Appl
35	32	56.1	778	3	US-08-808-599A-5	Sequence 5, Appl
36	32	56.1	1958	1	US-07-945-283-2	Sequence 2, Appl
37	32	56.1	8	3	US-08-434-099A-37	Sequence 37, Appl
38	31	54.4	15	4	US-08-860-808E-1	Sequence 1, Appl
39	31	54.4	15	3	US-08-469-141A-24	Sequence 24, Appl
40	31	54.4	15	5	PCT-US95-11794-24	Sequence 24, Appl
41	31	54.4	22	3	US-08-469-141A-52	Sequence 52, Appl
42	31	54.4	22	5	PCT-US95-11794-52	Sequence 52, Appl
43	31	54.4	29	1	US-08-507-016-3	Sequence 3, Appl
44	31	54.4	29	1	US-08-507-016-3	Sequence 3, Appl
45	31	54.4	29	1	US-08-507-016-3	Sequence 4, Appl

ALIGNMENTS

```

RESULT 1
US-08-905-310-12
; Sequence 12, Application US/08905310
; Patent No. 6072939
; GENERAL INFORMATION:
; APPLICANT: Wei, Ziping
; APPLICANT: Menon-Rudolph, Sunitha
; APPLICANT: Ghosh-Basildar, Pradip
; TITLE OF INVENTION: Polypeptides Having a Single Covalently Bound
; TITLE OF INVENTION: N-Terminal Water-Soluble Polymer, and Related Methods,
; FILE REFERENCE: SEQUENCE LISTING CRT 843
; CURRENT APPLICATION NUMBER: US/08/905,310
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 12
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism:peptide fragment
US-08-905-310-12

Query Match      100.0%; Score 57; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPRVHERHQA 11
      |||||
Db      1 GPRVHERHQA 11

RESULT 2
US-08-551-356-4
; Sequence 4, Application US/08551356
; Patent No. 5830700
; GENERAL INFORMATION:
; APPLICANT: Iranli, Meher
; TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: ZymoGenetics, Inc.
; STREET: 4225 Roosevelt Way, N.E.
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

```

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/551,356
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/349,762
FILING DATE:
APPLICATION NUMBER: US/07/998,271
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Holly, Julie A
REGISTRATION NUMBER: 33-246
REFERENCE/DOCKET NUMBER: 92-26
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 643 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-551-356-4

Query Match
Best Local Similarity 100.0%; Score 57; DB 2; Length 643;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPRVERHQSA 11
Db 36 GPRVERHQSA 46

RESULT 3
PCT-US93-12687-4
Sequence 4, Application PC/TUS9312687
GENERAL INFORMATION:
APPLICANT: Iran, Meher H.
TITLE OF INVENTION: HYBRID CROSS-LINKING PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12687
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/998,271
FILING DATE: 31-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 92-26PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 643 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-12687-4

Query Match
Best Local Similarity 100.0%; Score 57; DB 5; Length 643;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPRVERHQSA 11
Db 36 GPRVERHQSA 46

RESULT 4
US-08-206-176-2
Sequence 2, Application US/08206176
Patent No. 5639940
GENERAL INFORMATION:
APPLICANT: Garner, Ian
APPLICANT: Dalrymple, Michael A
APPLICANT: Prunkard, Donna E
APPLICANT: Foster, Donald C
TITLE OF INVENTION: Production of Fibrinogen in Transgenic
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,176
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 644 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-206-176-2

Query Match
Best Local Similarity 100.0%; Score 57; DB 1; Length 644;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPRVERHQSA 11
Db 36 GPRVERHQSA 46

RESULT 5
US-09-373-157-4
Sequence 4, Application US/09373157
Patent No. 6416963
GENERAL INFORMATION:
APPLICANT: Grieninger, Gerd
APPLICANT: Applegate, Dianne
APPLICANT: Stoike-Steben, Lara

;; TITLE OF INVENTION: NOVEL CLEAVED FRAGMENTS OF FIBRINOGEN
;; FILE REFERENCE: Sequence ID No. 6416963. 1-7 for 454-24
;; Patent No. 6416963
;; CURRENT APPLICATION NUMBER: US/09/373,157
;; CURRENT FILING DATE: 1999-08-12
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 4
;; LENGTH: 847
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-373-157-4

Query Match 100.0%; Score 57; DB 4; Length 847;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRVERHOSA 11
Db 17 GPRVERHOSA 27

RESULT 6
US-08-448-547-2
; Sequence 2, Application US/08448547
; Patent No. 5821068
; GENERAL INFORMATION:
; APPLICANT: Soe, Gilbu
; APPLICANT: Kohno, Isao
; APPLICANT: Imazuka, Kimiko
; APPLICANT: Ito, Yumiko
; TITLE OF INVENTION: ANTI-HUMAN SOLUBLE FIBRIN ANTIBODY,
; TITLE OF INVENTION: HYBRIDOMA, AND IMMUNOSSAYING METHOD
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MIOM, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,547
; FILING DATE: 30-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/01844
; FILING DATE: 01-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-297325
; FILING DATE: 02-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: Q-38931
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-448-547-2
Query Match 93.0%; Score 53; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPRVERHOS 10
Db 1 GPRVERHOS 10

RESULT 7
US-08-595-718A-5
; Sequence 5, Application US/08595718A
; Patent No. 5723579
; GENERAL INFORMATION:
; APPLICANT: Buettner, Joseph A.
; APPLICANT: Dadd, Christopher A.
; APPLICANT: Baumbach, George A.
; APPLICANT: Hammond, David J.
; TITLE OF INVENTION: Fibrinogen Binding Peptides
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 800 Dwight Way
; STREET: P. O. Box 1986
; CITY: Berkeley
; STATE: California
; COUNTRY: USA
; ZIP: 94701-1986
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb Storage
; COMPUTER: IBM
; OPERATING SYSTEM: DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,718A
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gibling, James A.
; REGISTRATION NUMBER: 25772
; REFERENCE/DOCKET NUMBER: MSB-7233
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510)705-7910
; TELEFAX: (510)705-7904
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: amino acid
; STRANDEDNESS: single strand
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: peptide
; PUBLICATION INFORMATION:
; AUTHORS: Kuvas, C.
; AUTHORS: Haeblerli, A.
; AUTHORS: Walder, P.
; AUTHORS: Straub, P. W.
; TITLE: Isolation of Human Fibrinogen and its
; TITLE: Derivatives by Affinity Chromatography on Gly-Pro-
; TITLE: Arg-Pro-Lys-Fractogel
; JOURNAL: Thromb. Haemost.
; VOLUME: 63
; ISSUE: 3
; PAGES: 439-444
; DATE: 28-JUN-1990
US-08-595-718A-5

Query Match 78.9%; Score 45; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.9e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRVVERHQ 9
DB 1 GPRVVERHK 9

RESULT 8

US-08-792-553-11
Sequence 11, Application US/08792553
Patent No. 5981200
GENERAL INFORMATION:
APPLICANT: Tsien, Roger Y.
TITLE OF INVENTION: Tandem Fluorescent Protein Constructs
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: FISH & RICHARDSON P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: California
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 31-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Hallie, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07257/041001/UC 96-160-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-792-553-11

Query Match 77.2%; Score 44; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPRVVERHK 8
DB 10 GPRVVERHK 17

RESULT 9

US-08-960-054A-10
Sequence 10, Application US/08960054A
Patent No. 6261537
GENERAL INFORMATION:
APPLICANT: Nycomed Imaging AS
TITLE OF INVENTION: Improvements in or relating to
TITLE OF INVENTION: diagnostic/therapeutic
FILE REFERENCE: REF/Klaveness/054
CURRENT APPLICATION NUMBER: US/08/960,054A
CURRENT FILING DATE: 1997-10-29
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: Sequence: Biotinylated
NAME/KEY: MOD_RES
LOCATION: (1)_RES
OTHER INFORMATION: Biotinylated-Gly
NAME/KEY: MOD_RES
LOCATION: (10)
OTHER INFORMATION: AMIDATION
US-08-960-054A-10

Query Match 71.9%; Score 41; DB 4; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.054;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GPRVVERHQ 10
DB 1 GPRVVERHQ 10

RESULT 10

US-08-958-993A-10
Sequence 10, Application US/08958993A
Patent No. 6264917
GENERAL INFORMATION:
APPLICANT: Nycomed Imaging AS
TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
FILE REFERENCE: REF/Klaveness/993
CURRENT APPLICATION NUMBER: US/08/958,993A
CURRENT FILING DATE: 1997-10-28
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Biotinylated
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: Biotinylated-Gly
NAME/KEY: MOD_RES
LOCATION: (10)
OTHER INFORMATION: AMIDATION
US-08-958-993A-10

Query Match 71.9%; Score 41; DB 4; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.054;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GPRVVERHQ 10
DB 1 GPRVVERHQ 10

RESULT 11

US-08-959-206A-7
Sequence 7, Application US/08959206A
Patent No. 6331289
GENERAL INFORMATION:
APPLICANT: Nycomed Imaging AS
TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
FILE REFERENCE: REF/Klaveness/206
CURRENT APPLICATION NUMBER: US/08/959,206A
CURRENT FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 10

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Biotinylated
OTHER INFORMATION: fibrin-antipolymerant peptide
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: Biotin-Gly
NAME/KEY: MOD_RES
LOCATION: (10)
OTHER INFORMATION: AMIDATION
US-08-959-206A-7

Query Match 71.9%; Score 41; DB 4; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.054;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPRVERHQS 10
Db 1 GPRPERHQS 10

RESULT 12
US-08-749-816-2
Sequence 2, Application US/08749816

PATENT No. 6013470
GENERAL INFORMATION:
APPLICANT: Lesage, Florian
APPLICANT: Guillemaire, Eric
APPLICANT: Fink, Michel
APPLICANT: Duprat, Fabrice
APPLICANT: Lazdunski, Michel
APPLICANT: Romey, Georges
APPLICANT: Barhanin, Jacques
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS
TITLE OF INVENTION: THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEISER & ASSOCIATES
STREET: 230 South Fifteenth Street, Suite 500
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,816
FILING DATE: 15-NOV-1996

CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:

NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 989.6351P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 336 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-749-816-2

Query Match 64.9%; Score 37; DB 3; Length 336;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVERHOSA 11
Db 12 RLVRRHSA 20

RESULT 13
US-09-144-914-2
Sequence 2, Application US/09144914

PATENT No. 6309855
GENERAL INFORMATION:
APPLICANT: Duprat, Fabrice
APPLICANT: Lesage, Florian
APPLICANT: Fink, Michel
APPLICANT: Lazdunski, Michel
TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
FILE REFERENCE: 989.6705CIP
CURRENT APPLICATION NUMBER: US/09/144,914
CURRENT FILING DATE: 1998-09-01
EARLIER APPLICATION NUMBER: 08/749,816
EARLIER FILING DATE: 1996-11-15
EARLIER APPLICATION NUMBER: 60/095,234
EARLIER FILING DATE: 1998-08-04
EARLIER APPLICATION NUMBER: FR 96/01565
EARLIER FILING DATE: 1996-02-08
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 336
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: TWIK-1
US-09-144-914-2

Query Match 64.9%; Score 37; DB 4; Length 336;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVERHOSA 11
Db 12 RLVRRHSA 20

RESULT 14
US-08-762-695-11
Sequence 11, Application US/08762695

PATENT No. 5846738
GENERAL INFORMATION:
APPLICANT: SEIDEL, CHRISTOPH
APPLICANT: BIALK, PETER
APPLICANT: VON DER ELTZ, HERBERT
TITLE OF INVENTION: SYNTHETIC STANDARD FOR IMMUNOASSAYS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY, AND ORAM
STREET: METROPOLITAN SQUARE, 655 15TH ST, N.W., SUITE
STREET: 330-G ST. LOBBY
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-5701

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,695
FILING DATE: 12-DEC-1996

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/325,589

```

FILING DATE: 19-OCT-1994
APPLICATION NUMBER: DE P 43 35 798.9
FILING DATE: 20-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 17 735.6
FILING DATE: 20-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 20 742.5
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: NOIAN, SHARON L.
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P1614.4050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-762-695-11

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Query Match      63.2%; Score 36; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 GPRVVER 7
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Db      1 GPRVVER 7

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RESULT 15
US-08-592-500-40
; Sequence 40, Application US/08592500
; Patent No. 6005069
; GENERAL INFORMATION:
; APPLICANT: Lanza, Francois
; APPLICANT: Phillips, David R.
; APPLICANT: Cazenave, Jean-Pierre
; TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,500
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,455
; FILING DATE: 09-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 12418-28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids

```

```

TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..11
OTHER INFORMATION: /note= "Amino acid sequence of the
OTHER INFORMATION: human fibrinogen (Fg) A-alpha 2 chain thrombin
FEATURE: cleavage site."
NAME/KEY: Region
LOCATION: 5..7
OTHER INFORMATION: /note= "Amino acid residues
OTHER INFORMATION: identical to GPV."
US-08-592-500-40

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Query Match      63.2%; Score 36; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 GPRVVER 7
        |||||
Db      5 GPRVVER 11

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Search completed: June 27, 2003, 17:19:03
Job time : 13.1 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 17:15:16 ; Search time 11.7 Seconds
(without alignments)
73.950 Million cell updates/sec

Title: US-10-019-439-2.

Perfect score: 51

Sequence: 1 GHRPLDKR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	31	2 A05297	fibrinogen beta ch
2	51	100.0	491	1 FGHUB	fibrinogen beta ch
3	43	84.3	468	1 FGBOR	fibrinogen beta ch
4	39	76.5	231	1 F64960	membrane protein y
5	39	76.5	231	2 D90966	hypothetical prote
6	39	76.5	231	2 D85814	hypothetical prote
7	39	76.5	673	2 T40817	zinc finger protei
8	38	74.5	463	2 A38463	fibrinogen beta ch
9	37	72.5	275	2 T04480	acyl-CoA oxidase h
10	36	70.6	195	2 C95286	probable transpos
11	36	70.6	201	2 C95399	probable transcrip
12	36	70.6	1490	2 T47840	multi resistance p
13	35	68.6	225	2 A75550	MutT/nudix family
14	35	68.6	571	2 AG3174	acetolactate synth
15	34	66.7	399	2 AE2616	hypothetical prote
16	34	66.7	402	2 E97398	hypothetical prote
17	34	66.7	419	2 T03675	probable oxygen-in
18	34	66.7	480	2 G75072	cyclin 2 - rice
19	34	66.7	736	2 T05137	prolyl-4RNA synth
20	34	66.7	795	2 A84608	protein kinase hom
21	34	66.7	862	2 B36786	hypothetical prote
22	33	64.7	155	2 S56258	hypothetical prote
23	33	64.7	162	2 S66764	hypothetical prote
24	33	64.7	250	2 T46417	hypothetical prote
25	33	64.7	403	2 T20727	hypothetical prote
26	33	64.7	424	2 D57742	cyclin III - maize
27	33	64.7	436	2 AB3419	sensor protein pho
28	33	64.7	464	2 H90340	hypothetical prote
29	33	64.7	485	2 F70464	hypothetical prote

30	33	64.7	501	2 H84727	probable inositol
31	33	64.7	570	2 G95326	probable acetolact
32	33	64.7	682	2 T18847	hypothetical prote
33	33	64.7	888	2 D84650	probable potassium
34	33	64.7	1058	2 D82654	ankyrin-like prote
35	32	62.7	127	2 G95281	hypothetical prote
36	32	62.7	142	2 S39708	ywdC protein - Bac
37	32	62.7	147	2 H69180	conserved hypotet
38	32	62.7	152	2 H90358	hypothetical prote
39	32	62.7	168	2 S78110	thi protein - Rhiz
40	32	62.7	183	2 AH0804	conserved hypotet
41	32	62.7	199	1 D33830	cation efflux syst
42	32	62.7	215	2 S23432	pyrogutamy1-pepti
43	32	62.7	222	2 H83387	probable hydrolase
44	32	62.7	262	2 B72333	bacteriocin - Ther
45	32	62.7	271	2 D70591	hypothetical prote

ALIGNMENTS

RESULT 1
A05297
Fibrinogen beta chain - dog (fragment)
C/Species: Canis lupus familiaris (dog)
C/Date: 05-Jun-1987 #sequence revision 05-Jun-1987 #text change 25-Oct-1996
C/Accession: B94308; A03123; A37512; A05297; B37512; D03118
R/Birken, S.; Wilner, G.D.; Canfield, R.E.
Thromb. Res. 7, 599-610, 1975
A/Title: Studies of the structure of canine fibrinogen.
A/Reference number: A94308; MUID:76081726; PMID:1198547
A/Accession: B94308
A/Molecule type: protein
A/Residues: 1-31 <BIR>
R/Blomback, B.; Blomback, M.; Groendahl, N.J.
Acta Chem. Scand. 19, 1789-1791, 1965
A/Title: Studies on fibrinopeptides from mammals.
A/Reference number: A03118
A/Accession: A03123
A/Molecule type: protein
A/Residues: 1-19 <BIO>
R/Krajewski, T.; Blomback, B.
Acta Chem. Scand. 22, 1339-1346, 1968
A/Reference number: A37512; MUID:6906367; PMID:5727635
A/Accession: A37512
A/Molecule type: protein
A/Residues: 1-19 <KRA>
C/Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf
C/Keywords: blood coagulation; liver; plasma; sulfoxprotein
F/1-19/Product: fibrinopeptide B #status experimental <APR>
F/2/Binding site: sulfate (Tyr) (covalent) #status experimental
F/3/Binding site: sulfate (Tyr) (covalent) #status experimental

Query Match 100.0%; Score 51; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHRPLDKR 9
Db 20 GHRPLDKR 28
|||||
|||

RESULT 2
FGHUB
Fibrinogen beta chain precursor [validated] - human
N/Alternate names: coagulation factor I
N/Contains: fibrinopeptide B
C/Species: Homo sapiens (man)
C/Date: 24-Apr-1984 #sequence revision 31-Mar-1993 #text change 08-Dec-2000
C/Accession: B43568; A90469; I37389; A94433; A90437; A94309; G54223; A03121; B3
R/Chung, D.W.; Harris, J.E.; Davie, E.W.
Adv. Exp. Med. Biol. 281, 39-48, 1990
A/Title: Nucleotide sequences of the three genes coding for human fibrinogen.

A/Reference number: A43568; MUID:91344740; PMID:2102623
 A/Accession: B43568
 A/Molecule type: DNA
 A/Residues: 9-191, 'P', 193-491 <CHU>
 R/Chung, D.W.; Que, B.G.; Rixton, M.W.; Mace Jr., M.; Davie, E.W.
 Biochemistry 22, 3244-3250, 1983
 A/Title: Characterization of complementary deoxyribonucleic acid and genomic deoxyribonucleic acid
 A/Reference number: A90469; MUID:83283433; PMID:6688356
 A/Accession: A90469
 A/Molecule type: DNA
 A/Residues: 1-38 <CH>
 A/Accession: B90469
 A/Molecule type: mRNA
 A/Residues: 9-191, 'A', 193-491 <CH2>
 A/Cross-references: GB:J00129; NID:G182429; PIDN:AA52429.1; PID:G182420
 R/Huber, P.; Dalmont, J.; Courtois, G.; Laurent, M.; Assouline, Z.; Marguerie, G.
 Nucleic Acids Res. 15, 1615-1625, 1987
 A/Title: Characterization of the 5'-flanking region for the human fibrinogen beta gene.
 A/Reference number: 137389; MUID:87146483; PMID:3029722
 A/Accession: 137389
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-38 <HUB>
 A/Cross-references: EMBL:X05018; NID:G31400; PIDN:CAA28674.1; PID:G31401
 R/Henschen, A.; Lottspeich, F.; Southan, C.; Topfer-Petersen, E.
 in Protides of the Biological Fluids, Proc. 28th Colloq., Peeters, H., ed., pp.51-56, Pe
 A/Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural v
 A/Reference number: A94433
 A/Accession: A94433
 A/Contents: carbohydrate binding
 A/Accession: A94433
 A/Molecule type: protein
 A/Residues: 31-137, 'QS', 140-144, 'QF', 147-491 <HEN>
 R/Watt, K.W.K.; Takagi, T.; Doolittle, R.F.
 Biochemistry 18, 68-76, 1979
 A/Title: Amino acid sequence of the beta chain of human fibrinogen.
 A/Reference number: A90437; MUID:79124640; PMID:420779
 A/Accession: A90437
 A/Molecule type: protein
 A/Residues: 31-144, 'QF', 147-231, 'D', 233-330, 'E', 332-491 <WAT>
 R/Biomback, B.; Hessel, B.; Hogg, D.
 Thromb. Res. 8, 639-658, 1976
 A/Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
 A/Reference number: A94309; MUID:76225080; PMID:936108
 A/Accession: A94309
 A/Contents: disulfide bonds
 A/Accession: A94309
 A/Molecule type: protein
 A/Residues: 31-112, 'E', 114-137, 'QS', 140-144, 'QF', 147-148 <BLO>
 R/Kuntlake, S.T.; Carilli, C.T.; Lau, K.; Procter, A.A.; Naya-Vigne, J.; Kane, J.P.
 Biochemistry 33, 1988-1993, 1994
 A/Title: Identification of proteins associated with apolipoprotein A-I-containing lipopr
 A/Reference number: A54223; MUID:94162201; PMID:8117655
 A/Accession: G54223
 A/Molecule type: protein
 A/Residues: 164-174 <KUN>
 A/Note: Identification of tryptic peptides from high-density lipoproteins
 R/Henschen, A.; Lottspeich, F.; Kehl, M.; Southan, C.
 Ann. N. Y. Acad. Sci. 408, 28-42, 1983
 A/Title: Covalent structure of fibrinogen.
 A/Reference number: A90037; MUID:83254370; PMID:6575689
 A/Contents: annotation; review, disulfide bonds
 R/Gardlund, B.; Hessel, B.; Marguerie, G.; Murano, G.; Blomback, B.
 Eur. J. Biochem. 77, 595-610, 1977
 A/Title: Primary structure of human fibrinogen. Characterization of disulfide-containing
 A/Reference number: A91249; MUID:7245999; PMID:891553
 A/Contents: annotation; disulfide bonds
 R/Doolittle, R.F.; Takagi, T.; Watt, K.; Bouma III, H.; Cottrell, B.A.; Caseman, K.G.; G
 A/Title: The structures of fibrinogen and their inhibitors, Magnusson, S., Ottesen, M., Fold
 A/Reference number: A94437
 A/Contents: annotation; disulfide bonds
 R/Doolittle, R.F.
 Annu. Rev. Biochem. 53, 195-229, 1984
 A/Title: Fibrinogen and fibrin.

A/Reference number: A90041; MUID:84305751; PMID:6389194
 A/Contents: annotation; review, EM structure, polymerization, ligands
 R/Chung, D.W.; Rixton, M.W.; Que, B.G.; Davie, E.W.
 Ann. N. Y. Acad. Sci. 408, 449-456, 1983
 A/Title: Cloning of fibrinogen genes and their cDNA.
 A/Reference number: A90038; MUID:83254384; PMID:6575700
 A/Contents: annotation
 R/Kirschbaum, N.E.; Budzynski, A.Z.
 J. Biol. Chem. 265, 13669-13676, 1990
 A/Title: A unique proteolytic fragment of human fibrinogen containing the Alpha COOH-
 A/Reference number: A37117; MUID:9033977; PMID:2143188
 A/Contents: annotation; hematin cleavage site
 A/Note: hematin, a protease from Haementeria ghilliani, the giant South American leech
 C/Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleav
 ization sites responsible for the formation of the soft clot.
 C/Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabil
 izer) and between alpha chains (weaker) of different monomers.
 C/Comment: All fibrinogen chains are synthesized in the liver.
 C/Genetics:
 A/Gene: GDB:FBG
 A/Cross-references: GDB:119130; OMIM:134830
 A/Map position: 4q28-4q28
 A/Intons: 38/3; 102/3; 164/1; 240/1; 278/1; 320/1; 415/2
 C/Complex: The fibrinogen molecule is a hexamer containing two sets of alpha (see PIR:F
 ins are contained in the core. Two three-chain coiled coils emerge from this core and c
 from the distal domain nodes.
 C/Function:
 A/Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
 A/Pathway: blood coagulation
 C/Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf
 C/Keywords: blood coagulation; coiled coil; glycoprotein; liver; plasma; pyroglyutamic a
 F/1-30/Domain: (or 4-30 or 15-30) signal sequence #status experimental <SIG>
 F/31-491/Product: fibrinogen beta chain #status experimental <MAT>
 F/31-44/Product: fibrinopeptide B #status experimental <MAT>
 F/45-491/Product: fibrin beta chain #status experimental <APT>
 F/45-47/Region: polymerization site
 F/99-228/Domain: fibrinogen disulfide ring homology <FDR>
 F/238-487/Domain: fibrinogen beta/gamma homology <FBG>
 F/31/Modified site: pyroglutamate carboxylic acid (Gln) (in mature form) #status experime
 F/44-45/Cleavage site: Arg-Gly (thrombin) #status experimental
 F/95/Disulfide bonds: interchain (to alpha-55) #status experimental
 F/106/Disulfide bonds: interchain (to alpha-68) #status experimental
 F/110/Disulfide bonds: interchain (to gamma-45) #status experimental
 F/223/Disulfide bonds: interchain (to gamma-184) #status experimental
 F/227/Disulfide bonds: interchain (to gamma-161) #status experimental
 F/231-316,241-270,424-437/Disulfide bonds: #status experimental
 F/394/Binding site: carbohydrate (Asn) (covalent) #status experimental
 Query Match 100.0%; Score 51; DB 1; Length 491;
 Best Local Similarity 100.0%; Pred. No. 0.036;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDKKR 9
 DB 45 GHRPLDKKR 53
 RESULT 3
 FGBOR
 fibrinogen beta chain - bovine
 N/Contrains: fibrinopeptide B
 C/Spectes: Bos primigenius taurus (cattle)
 C/Date: 29-Jul-1981 #sequence revision 29-Jul-1991 #text_change 13-Sep-1996
 C/Accession: A03122; B03117; B37507; A37513; S02443
 R/Blomback, B.; Doolittle, R.F.
 Acta Chem. Scand. 17, 1816-1819, 1963
 A/Title: The sequence of amino acids at the N-terminal end of bovine fibrinopeptide B.
 A/Reference number: A03122
 A/Accession: A03122
 A/Molecule type: protein
 A/Residues: 1-4 <BLO>
 R/Stojquist, J.; Blomback, B.; Wallen, P.
 Ark. Kemi 16, 425-436, 1960

A>Title: Amino acid sequence of bovine fibrinopeptides.
 A/Accession number: A03117
 A/Accession: B03117
 A/Molecule type: protein
 A/Residues: 5-21 <SUO>
 R/Martinielli, R.A.; Ingalls, A.S.; Rubira, M.R.; Hageman, T.C.; Hurrell, J.G.R.; Leach, S.
 Arch. Biochem. Biophys. 192, 27-32, 1979
 A>Title: Amino acid sequences of portions of the alpha and beta chains of bovine fibrin
 A/Reference number: A37507; MUID:79164394; PMID:434821
 A/Accession: B37507
 A/Molecule type: protein
 A/Residues: 22-53 <MAK>
 R/Chung, D.W.; Rixon, M.W.; MacGillivray, R.T.A.; Davie, E.W.
 Proc. Natl. Acad. Sci. U.S.A. 78, 1466-1470, 1981
 A>Title: Characterization of a cDNA clone coding for the beta chain of bovine fibrinogen
 A/Reference number: A37513; MUID:81199473; PMID:6262803
 A/Accession: A37513
 A/Molecule type: mRNA
 A/Residues: 44-468 <CHU>
 R/Medved, L.V.; Platonova, T.N.; Litvinovich, S.V.; Lukinova, N.I.
 FEBS Lett. 232, 56-60, 1988
 A>Title: The cleavage of beta-chain in bovine fibrinogen D(H) fragment (95 kDa) leads to
 A/Reference number: S02443; MUID:88211875; PMID:2966748
 A/Accession: S02443
 A/Molecule type: protein
 A/Residues: 373-374 <MED>
 C/Comment: Thrombin cleaves the bond between Arg-21 and Gly-22 to release fibrinopeptide
 C/Comment: Fibrinogen is a hexamer containing two sets of three nonidentical chains (alpha
 C/Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide
 C/Keywords: blood coagulation; glycoprotein; plasma; pyroglyutamic acid; sulfoprotein
 F/76-205/Domain: fibrinogen disulfide ring homology <FDR>
 F/215-464/Domain: fibrinogen beta/gamma homology <FBG>
 F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F/6/Binding site: sulfate (Tyr) (covalent) #status experimental
 F/21-22/Cleavage site: Arg-Gly (thrombin) #status experimental
 F/371/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F/372-373/Cleavage site: Arg-Thr (plasmin) #status experimental

Query Match 84.3%; Score 43; DB 1; Length 468;
 Best Local Similarity 77.8%; Pred. No. 1.3;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDKKR 9
 DB 22 GHRPLDKKR 30

RESULT 4
 F64960
 membrane protein yedJ - Escherichia coli (strain K-12)
 C/Species: Escherichia coli
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 01-Mar-2002
 A/Accession: F64960
 R/Battler, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A>Title: The complete genome sequence of Escherichia coli K-12.
 A/Reference number: A64720; MUID:97426617; PMID:9278503
 A/Accession: F64960
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-231 <BLAT>
 A/Cross-references: GB:AE000288; GB:U00096; NID:g2367124; PIDN:ANC75028.1; PID:g1788273;
 A/Experimental source: strain K-12, substrain MG1655
 C/Genetics:
 A/Gene: yedJ
 C/Superfamily: conserved hypothetical protein AF0994
 C/Keywords: transmembrane protein
 F/48-64/Domain: transmembrane #status predicted <TM1>
 F/135-151/Domain: transmembrane #status predicted <TM2>

Query Match 76.5%; Score 39; DB 1; Length 231;
 Best Local Similarity 87.5%; Pred. No. 4;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPIDDKR 9
 DB 161 HRPIDDKR 168

RESULT 7
 T40817
 zinc finger protein - fission yeast (Schizosaccharomyces pombe)
 C/Species: Schizosaccharomyces pombe
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Sep-2000
 A/Accession: T40817

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPIDDKR 9
 DB 161 HRPIDDKR 168

RESULT 5
 D90966
 hypothetical protein Ec2700 [imported] - Escherichia coli (strain O157:H7, substrain R
 C/Species: Escherichia coli
 C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
 A/Accession: D90966
 R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 gaswara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hartori, M.; Shinagawa, H.
 DNA Res. 9, 11-22, 2001
 A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
 A/Reference number: A9629; MUID:21156231; PMID:11258796
 A/Accession: D90966
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-231 <HAV>
 A/Cross-references: GB:BA000007; PIDN:BA836123.1; PID:g13362168; GSPDB:GN00154
 A/Experimental source: strain O157:H7, substrain R1MD 0509952
 C/Genetics:
 A/Gene: Ec2700
 C/Superfamily: conserved hypothetical protein AF0994

Query Match 76.5%; Score 39; DB 2; Length 231;
 Best Local Similarity 87.5%; Pred. No. 4;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPIDDKR 9
 DB 161 HRPIDDKR 168

RESULT 6
 D85814
 hypothetical protein yedJ [imported] - Escherichia coli (strain O157:H7, substrain EDL9
 C/Species: Escherichia coli
 C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
 A/Accession: D85814
 R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe
 iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca
 Nature 409, 529-533, 2001
 A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A/Reference number: A85480; MUID:21074935; PMID:11206551
 A/Accession: D85814
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-231 <STO>
 A/Cross-references: GB:AE005174; NID:g12516071; PIDN:AGS6976.1; GSPDB:GN00145; UWGP:23
 A/Experimental source: strain O157:H7, substrain EDL933
 C/Genetics:
 A/Gene: yedJ
 C/Superfamily: conserved hypothetical protein AF0994

Query Match 76.5%; Score 39; DB 2; Length 231;
 Best Local Similarity 87.5%; Pred. No. 4;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPIDDKR 9
 DB 161 HRPIDDKR 168

R.Beck, A.; Reinhardt, R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, October 1998
 A:Reference number: Z21949
 A:Accession: T40817
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-673 <BEC>
 A:Cross-references: EMBL:AL032684; PIDN:CAA21808.1; GSPDB:GN00067; SPDB:SPBP887.23
 A:Experimental source: strain 972h; clone pl p887
 C:Genetics:
 A:Gene: SPDB:SPBP87.23
 A:Map position: 2
 C:Superfamily: RING finger homology
 F:210-278/Domain: RING finger homology <RRN>

Query Match
 Best Local Similarity 76.5%; Score 39; DB 2; Length 673;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 GHRPLDKR 9
 Db 160 GHRPLDKR 168

RESULT 8
 A38463
 fibrinogen beta chain - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C>Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 13-Aug-1999
 C:Accession: A38463
 R:Weisbach, L.; Oddoux, C.; Procyk, R.; Grieninger, G.
 Biochemistry 30, 3290-3294, 1991
 A:Title: The beta chain of chicken fibrinogen contains an atypical thrombin cleavage site
 A:Reference number: A38463; MUID:91182745; PMID:2009266
 A:Accession: A38463
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-463 <WEI>
 A:Cross-references: GB:M58514; NID:9211779; PIDN:AAA48770.1; PID:9211780
 C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide
 F:73-202/Domain: fibrinogen disulfide ring homology <FDR>
 F:212-460/Domain: fibrinogen beta/gamma homology <FBG>

Query Match
 Best Local Similarity 74.5%; Score 38; DB 2; Length 463;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 2 HRPDLKRR 9
 Db 19 HRPDLKRR 26

RESULT 9
 T04480
 acyl-CoA oxidase homolog - barley (fragment)
 C:Species: Hordeum vulgare (barley)
 C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
 C:Accession: T04480
 R:Grossi, M.; Gullit, M.; Stanca, A.M.; Cattiveili, L.
 Plant Sci. 105, 71-80, 1995
 A:Title: Characterization of two barley genes that respond rapidly to dehydration stress
 A:Reference number: Z15371
 A:Accession: T04480
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-275 <GRO>
 A:Cross-references: EMBL:X84055; NID:9642243; PIDN:CAA58874.1; PID:9642244
 A:Experimental source: cv. Arda, leaf
 C:Genetics:
 A:Gene: cdc29

Query Match
 Best Local Similarity 72.5%; Score 37; DB 2; Length 275;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Oy 2 HRPDLKRR 9
 Db 19 HRPDLKRR 26

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 GHRPLDKR 9
 Db 225 GHRPLDKR 233

RESULT 10
 C95286
 Probable transposase [imported] - Sinorhizobium meliloti (strain 1021) megaplasmid pSym
 C:Species: Sinorhizobium meliloti
 C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: C95286
 R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bow
 .; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilo
 A:Reference number: A95262; MUID:21396509; PMID:11481432
 A:Accession: C95286
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-195 <KUR>
 A:Cross-references: GB:AE006469; PIDN:AAK64853.1; PID:914523267; GSPDB:GN00165
 A:Experimental source: strain 1021, megaplasmid pSym
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
 .; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
 .; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K
 A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: SMA0360
 A:Genome: plasmid

Query Match
 Best Local Similarity 70.6%; Score 36; DB 2; Length 195;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 GHRPLDKR 9
 Db 46 GHRPLDKR 54

RESULT 11
 C95399
 Probable transcription regulator [imported] - Sinorhizobium meliloti (strain 1021) mag
 C:Species: Sinorhizobium meliloti
 C>Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: C95399
 R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bow
 .; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilo
 A:Reference number: A95262; MUID:21396509; PMID:11481432
 A:Accession: C95399
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-201 <KUR>
 A:Cross-references: GB:AE006469; PIDN:AAK65757.1; PID:914524255; GSPDB:GN00165
 A:Experimental source: strain 1021, megaplasmid pSym
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler
 .; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
 .; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K
 A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:

A:Gene: SMA2008
A:Genome: plasmid

Query Match 70.6%; Score 36; DB 2; Length 201;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
|||
Db 175 GHRPLD 180

RESULT 12

17840
multi resistance protein homolog - Arabidopsis thaliana
N:Alternate names: protein T209.140

C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 21-Jul-2000
R:Yakutara, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
submitted to the Protein Sequence Database, February 2000
A:Reference number: Z24475
A:Accession: T47840

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1490 <NTA>
A:Cross-references: EMBL:AL138658
A:Experimental source: cultivar Columbia; BAC clone T209

A:Map position: 3
A:introns: 9/1; 795/3; 824/3; 1036/3; 1075/3; 1174/1; 1245/3; 1347/3; 1369/1; 1449/1
A:Note: T209.140
C:Superfamily: human multidrug resistance protein CMOAT2; ATP-binding cassette homology

Query Match 70.6%; Score 36; DB 2; Length 1490;
Best Local Similarity 100.0%; Pred. No. 1; Indels 0; Gaps 0;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GHRPLD 6
|||
Db 1226 GHRPLD 1231

RESULT 13

A75550
Mult/indix family protein - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: A75550

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75550; PMID:20036896; PMID:10567266
A:Accession: A75550

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-225 <WHI>
A:Cross-references: GB:AE001881; GB:AE000513; NID:96457853; PIDN:AAF09779.1; PID:9645786
A:Experimental source: strain R1
C:Genetics:

A:Gene: DR0192
A:Map position: 1
Query Match 68.6%; Score 35; DB 2; Length 225;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 8
|||
Db 178 GHRPLDKR 185

RESULT 14

AG3174

acetylactate synthase [imported] - Agrobacterium tumefaciens (strain C58, Dupont) plasmid
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002

C:Accession: AG3174
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; Mccliel
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193

A:Accession: AG3174
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-571 <KUR>
A:Cross-references: GB:AE008687; PIDN:AA145813.1; PID:G17743551; GSPDB:GN00188
A:Experimental source: strain C58 (Dupont)
C:Genetics:

A:Gene: atic
A:Genome: plasmid
C:Superfamily: acetylactate synthase large chain; thiamin pyrophosphate-binding domain

Query Match 68.6%; Score 35; DB 2; Length 571;
Best Local Similarity 66.7%; Pred. No. 63;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDKR 9
|||
Db 183 GHRPLDKR 191

RESULT 15

AE2616

hypothetical protein hemm [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002

C:Accession: AE2616
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; Mccliel
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193

A:Accession: AE2616
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-399 <KUR>
A:Cross-references: GB:AE008688; PIDN:AA141347.1; PID:G17738661; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:

A:Gene: hemm
A:Map position: circular chromosome
C:Superfamily: oxygen-independent coproporphyrinogen oxidase

Query Match 66.7%; Score 34; DB 2; Length 399;
Best Local Similarity 62.5%; Pred. No. 69;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPLDKR 9
|||
Db 47 HRPLDKR 54

Search completed: June 27, 2003, 17:18:36
Job time : 12.7 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 17:13:51 ; Search time 6.3 Seconds
(without alignments)
59.252 Million cell updates/sec

Title: US-10-019-439-2
Perfect score: 51
Sequence: 1 GHRPLDKKR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	51	100.0	31	1 FIBB_CANFA
2	51	100.0	491	1 FIBB_HUMAN
3	43	84.3	468	1 FIBB_BOVIN
4	39	76.5	231	1 YEDJ_ECOLI
5	39	76.5	479	1 FIBB_RAT
6	38	74.5	463	1 FIBB_CHICK
7	36	70.6	333	1 MWAM_ZYMO
8	34	66.7	256	1 CSEN_HUMAN
9	34	66.7	419	1 CG2B_ORYSA
10	34	66.7	862	1 VGO1_HSV1
11	34	66.7	3317	1 CADN_RAT
12	34	66.7	3354	1 CADN_HUMAN
13	34	66.7	3354	1 CADN_MOUSE
14	33	64.7	81	1 YQ72_BACAN
15	33	64.7	155	1 YFH3_YEAS
16	32	62.7	142	1 YWDC_BACSU
17	32	62.7	147	1 Y609_METH
18	32	62.7	215	1 PCP_EACSU
19	32	62.7	271	1 YW34_MYCTU
20	32	62.7	316	1 CZCD_ALCEP
21	32	62.7	316	1 CZCD_ALCEP
22	32	62.7	336	1 YW95_YEAS
23	32	62.7	436	1 CRTI_ERMHE
24	32	62.7	560	1 ERS_MOUSE
25	32	62.7	677	1 SKD3_MOUSE
26	32	62.7	1052	1 RPOC_BACAN
27	32	62.7	1080	1 HD44_CHICK
28	32	62.7	1084	1 HD44_HUMAN
29	32	62.7	1209	1 THR_DROME
30	31	60.8	75	1 RS2B_MERLA
31	31	60.8	168	1 MBP_RABIT
32	31	60.8	169	1 MBP_BOVIN
33	31	60.8	212	1 TPAI_AGRTU

34	31	60.8	351	1 DESA_SYNY3	P20388 synechocyst
35	31	60.8	363	1 TRMA_PSEFL	Q9rth9 pseudomonas
36	31	60.8	374	1 TGT_SYNY3	O55983 synechocyst
37	31	60.8	381	1 KCRM_CHICK	P00565 gallus gall
38	31	60.8	404	1 ISCS_MERTE	P57795 methanosarc
39	31	60.8	408	1 CH60_RICRI	O34198 ticketstia
40	31	60.8	424	1 THC2_METH	O27617 methanobact
41	31	60.8	424	1 Y963_PYRHO	O58701 pyrococcus
42	31	60.8	426	1 CH60_RICRY	O85754 rickettsia
43	31	60.8	434	1 CG2B_MEDVA	P46278 medicago va
44	31	60.8	517	1 CAIC_SALTI	O82914 salmonella
45	31	60.8	517	1 CAIC_SALTY	O82914 salmonella

ALIGNMENTS

RESULT 1	FIBB_CANFA	STANDARD;	PRT;	31 AA.
AC	P02677;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-OCT-1989 (Rel. 12, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).			
GN	FGB.			
OS	Canis familiaris (Dog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
OX	NCBI_TaxID=9615;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=76081726; PubMed=1198547;			
RA	Birken S., Wilner G.D., Canfield R.E.;			
RT	"Studies of the structure of canine fibrinogen.";			
RL	Thromb. Res. 7:599-610 (1975).			
RN	[2]			
RP	SEQUENCE OF 1-19.			
RA	Blomback B., Grondahl N.J.;			
RT	"Studies on fibrinopeptides from mammals.";			
RL	Acta Chem. Scand. 19:1789-1791 (1965).			
RN	[3]			
RP	SEQUENCE OF 1-19.			
RX	MEDLINE=69066367; PubMed=5727635;			
RA	Krajewski T., Blomback B.;			
RT	"The location of tyrosine-O-sulphate in fibrinopeptides.";			
RL	Acta Chem. Scand. 22:1339-1346 (1968).			
CC	-1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION.			
CC	-1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.			
CC	-1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.			
CC	PIR; A03123; A03123.			
DR	PIR; A05297; A05297.			
DR	Interpro; IPR002181; Fibrinogen C.			
DR	PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.			
KW	Blood coagulation; Plasma; Sulfation.			
FT	PEPTIDE 1 19 FIBRINOPEPTIDE B.			
FT	MOD_RES 20 >31 FIBRINOGEN BETA CHAIN.			
FT	MOD_RES 2 2 SULFATION (IN B[2] CHAIN).			
FT	MOD_RES 3 3 SULFATION (IN B[1] & B[2] CHAINS).			
FT	NON_TER 31			
FT	NON_TER 31			
SQ	SEQUENCE 31 AA; 3731 MW; A043727257698156 CRC64;			
Query Match	100.0%;	Score 51;	DB 1;	Length 31;
Best Local Similarity	100.0%;	Pred. No. 0.00054;		
Matches 9;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	1 GHRPLDKKR 9			

DB 20 GHRPLDKR 28

RESULT 2
FIBB_HUMAN STANDARD; PRT; 491 AA.
ID P02675;
AC 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
GN FGB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=91344740; PubMed=2102623;
RA Chung D.W., Harris J.E., Davie E.W.;
RT "Nucleotide sequences of the three genes coding for human
RL fibrinogen.";
RN Adv. Exp. Med. Biol. 281:39-48(1990).
RP SEQUENCE FROM N.A.
RX MEDLINE=8328433; PubMed=6688356;
RA Chung D.W., Que B.G., Rixon M.W., Mace M. Jr., Davie E.W.;
RT "Characterization of complementary deoxyribonucleic acid and genomic
RL deoxyribonucleic acid for the beta chain of human fibrinogen.";
RN Biochemistry 22:3244-3250(1983).
RP SEQUENCE FROM N.A.
RA Chung D.W., Harris J.E., Davie E.W.;
RT "Nucleotide sequences of the three genes coding for human
RL fibrinogen.";
RN (in) Liu C.Y., Chien S. (eds.);
RL Fibrinogen, thrombosis, coagulation and fibrinolysis, pp.39-48,
PLenum Press, New York (1991).
RN
RP SEQUENCE FROM N.A., AND VARIANTS SRR-100; HIS-170; LEU-265 AND
LYS-478.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RN Nickerson D.A.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBD databases.
RN
RP SEQUENCE OF 31-491, AND CARBOHYDRATE-LINKAGE SITE.
RA Henschen A., Lotsepelch F., Southan C., Topfer-Petersen E.;
RT "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
RL structural variants.";
RN (in) Peeters H. (eds.);
RL Provides of the biological fluids, Proc. 28th colloquium, pp.51-56,
PL Pergamon Press, Oxford (1980).
RN
RP SEQUENCE OF 31-491.
RX MEDLINE=79124640; PubMed=420779;
RA Watt K.W.K., Takagi T., Doolittle R.F.;
RT "Amino acid sequence of the beta chain of human fibrinogen.";
RN Biochemistry 18:68-76(1979).
RP
RP SEQUENCE OF 31-148, AND DISULFIDE BONDS.
RX MEDLINE=7625080; PubMed=936108;
RA Blomback B., Hessel B., Hogg D.;
RT "Disulfide bridges in NH2-terminal part of human fibrinogen.";
RN Thromb. Res. 8:639-658(1976).
RP
RP SEQUENCE OF 1-38 FROM N.A.
RX MEDLINE=87146483; PubMed=3029722;
RA Huber P., Dalmont J., Courtois G., Laurent M., Assouline Z.,
RT Marguerie G.;
RN "Characterization of the 5'-flanking region for the human fibrinogen
beta gene.";
RL Nucleic Acids Res. 15:1615-1625(1987).
RN
RP SEQUENCE OF 31-44.
RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
RT "Studies on fibrinopeptides from primates.";
RN Acta Chem. Scand. 19:1788-1789(1965).
RN
RP REVIEW, AND DISULFIDE BONDS.
RX MEDLINE=83254370; PubMed=6575689;
RA Henschen A., Lotsepelch F., Kehl M., Southan C.;
RT "Covalent structure of fibrinogen.";
RN Ann. N.Y. Acad. Sci. 408:28-43(1983).
RN
RP DISULFIDE BONDS.
RX MEDLINE=7724599; PubMed=891553;
RA Gaardlund B., Hessel B., Marguerie G., Murano G., Blomback B.;
RT "Primary structure of human fibrinogen. Characterization of
RL disulfide-containing cyanogen-bromide fragments.";
RN Eur. J. Biochem. 77:595-610(1977).
RN
RP DISULFIDE BONDS.
RX Doolittle R.F., Takagi T., Watt K.W.K., Bouma H. III, Cottrell B.A.,
RA Cassman K.G., Goldbaum D.W., Doolittle L.R., Fritzen S.J.;
RT "The structures of fibrinogen and fibrin.";
RN (in) Magnusson S., Ottesen M., Foltmann B., Dano K.,
RL Neurath H. (eds.);
RN Regulatory proteolytic enzymes and their inhibitors, pp.163-172,
PL Pergamon Press, New York (1978).
RN
RP REVIEW, FM STRUCTURE, POLYMERIZATION, AND LIGANDS.
RX MEDLINE=84305751; PubMed=6383194;
RA Doolittle R.F.;
RN "Fibrinogen and fibrin.";
RN Annu. Rev. Biochem. 53:195-229(1984).
RN
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 164-491.
RX MEDLINE=97472408; PubMed=933233;
RA Spraggon G., Everse S.J., Doolittle R.F.;
RT "Crystal structures of fragment D from human fibrinogen and its
RL crosslinked counterpart from fibrin.";
RN Nature 389:455-462(1997).
RN
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 164-491.
RX MEDLINE=98292395; PubMed=9628725;
RA Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
RT "Crystal structure of fragment double-D from human fibrin with two
RL different bound ligands.";
RN Biochemistry 37:8637-8642(1998).
RN
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=99175089; PubMed=10074346;
RA Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
RT "Conformational changes in fragments D and double-D from human
RL fibrinogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
RN Biochemistry 38:2941-2946(1999).
RN
RP VARIANT BALTIMORE-2.
RX MEDLINE=89058942; PubMed=3194892;
RA Schmelzer C.H., Ebert R.F., Bell W.R.;
RT "A polymorphism at B beta 448 of fibrinogen identified during
RL structural studies of fibrinogen Baltimore II.";
RN Thromb. Res. 52:173-177(1988).
RN
RP VARIANT ISE.
RX MEDLINE=91208409; PubMed=2018836;
RA Yoshida N., Wada H., Morita K., Hirata H., Matsuda M., Yamazumi K.,
RT Asakura S., Shirakawa S.;
RN "A new congenital abnormal fibrinogen Ise characterized by the
replacement of B beta glycine-15 by cysteine.";
RL Blood 77:1958-1963(1991).
RN
RP VARIANT NAPLES.
RX MEDLINE=92340664; PubMed=1634610;
RA Koopman J., Haverkate F., Lord S.T., Grimbergen J., Mannucci P.M.;

RT "Molecular basis of fibrinogen Naples associated with defective
RT thrombin binding and thrombophilia. Homozygous substitution of B beta
RT 68 Ala->Thr.";
RT J. Clin. Invest. 90:238-244 (1992).
RN [20]
RP VARIANTS IUMIDEN AND NIJMEGEN.
RX MEDLINE=92228809; PubMed=1565641;
RA Koopman J., Haverkate F., Grimbergen J., Engesser L., Novakova I.,
RA Kerst A.F.J.A., Lord S.T.;
RT "Abnormal fibrinogens Iumiden (B beta Arg14-->Cys) and Nijmegen (B
RT beta Arg4-->Cys) form disulfide-linked fibrinogen-albumin
RT complexes";
RT Proc. Natl. Acad. Sci. U.S.A. 89:3478-3482 (1992).
RN [21]
RP VARIANT NEW YORK-1.
RX MEDLINE=85157605; PubMed=3156856;
RA Liu C.Y., Koehn J.A., Morgan F.J.;
RT "Characterization of fibrinogen New York 1. A dysfunctional
RT fibrinogen with a deletion of B beta (9-72) corresponding exactly to
RT exon 2 of the gene";
RT J. Biol. Chem. 260:4390-4396 (1985).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC THE AMINO ENDS OF ALL CHAINS ARE CONTAINED IN THE CENTRAL NODULE.
CC DIVERGING FROM THIS NODULE ARE 2 THREE-CHAIN COILED COILS WHICH
CC CONNECT THE CENTRAL NODULE TO THE DISTAL NODULES CONTAINING THE
CC DISTAL DOMAINS. EXTENDING FAR PERIPHERALLY ARE THE LONG CARBOXYL
CC ENDS OF THE ALPHA CHAINS.
CC -1- DISEASE: DEFECTS IN FGB ARE A CAUSE OF THROMBOPHILIA.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THIS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CC CONVERTED INTO THE HARD CLOT BY FACTOR XIIIa WHICH CATALYZES THE
CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
CC MONOMERS.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC -----
DR EMBL: J00129; AAA52429.1; -;
DR EMBL: J00131; AAA98115.1; -;
DR EMBL: J00130; AAA98115.1; JOINED.
DR EMBL: J00132; AAA98116.1; -;
DR EMBL: J00133; -; NOT ANNOTATED_CDS.
DR EMBL: AF388026; AA62470.1; -;
DR EMBL: X05018; CAA28674.1; -;
DR EMBL: M64983; AAA18024.2; -;
DR EMBL: M26877; AAA52445.1; -;
DR EMBL: M26876; AAA52445.1; JOINED.
CC
Query Match 100.0%; Score 51; DB 1; Length 491;
Best Local Similarity 100.0%; Score No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 GHRPLDKR 9
DB 45 GHRPLDKR 53
RESULT 3
FIBR_BOVIN STANDARD; PRT; 468 AA.
ID FIBR_BOVIN

AC P02676;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
GN FGB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bos.
OX NCBI_TaxId=9913;
RN [1]
RP SEQUENCE OF 1-4.
RA Blomback B., Doolittle R.F.;
RT "The sequence of amino acids at the N-terminal end of bovine
RT fibrinopeptide B.";
RT Acta Chem. Scand. 17:1816-1819 (1963).
RN [2]
RP SEQUENCE OF 5-21.
RA Sjoquist J., Blomback B., Wallen P.;
RT "Amino acid sequence of bovine fibrinopeptides";
RT Ark. Kent 16:425-436 (1960).
RN [3]
RP SEQUENCE OF 22-53.
RX MEDLINE=79164394; PubMed=434821;
RA Martelli R.A., Inglis A.S., Rubira M.R., Hagaman T.C.,
RA Hartnell J.G.R., Leach S.J., Scheraga H.A.;
RT "Amino acid sequences of portions of the alpha and beta chains of
RT bovine fibrinogen";
RT Arch. Biochem. Biophys. 192:27-32 (1979).
RN [4]
RP SEQUENCE OF 44-468 FROM N.A.
RX MEDLINE=81199473; PubMed=6262803;
RA Chung D.W., Rixon M.W., McGillivray R.T.A., Davie E.W.;
RT "Characterization of a cDNA clone coding for the beta chain of bovine
RT fibrinogen";
RT Proc. Natl. Acad. Sci. U.S.A. 78:1466-1470 (1981).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THIS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CC CONVERTED INTO THE HARD CLOT BY FACTOR XIIIa WHICH CATALYZES THE
CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
CC MONOMERS.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC -----
DR EMBL: V00110; CAA23444.1; -;
DR PIR: A03122; FGBOB.
DR HSP: P02675; 1FZB.
DR InterPro: IPR002181; Fibrinogen.C.
DR Pfam: PF00147; Fibrinogen.C.1.
DR SMART: SM00186; FGB; 1.
DR PROSITE: PS00514; FIBRIN AG C DOMAIN; 1.
KW Blood coagulation; Plasma; Platelet; Glycoprotein; Sulfation.
FT PEPTIDE 1 21
FT CHAIN 22 468 FIBRINOGEN BETA CHAIN.
FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD RES 6 6 SULFATION.
FT SITE 21 22 CLEAVAGE (BY THROMBIN; RELEASE

FT DISULFID 72 72 FIBRINOPEPTIDE B).
 FT DISULFID 83 83 INTERCHAIN (WITH ALPHA).
 FT DISULFID 87 87 INTERCHAIN (WITH ALPHA).
 FT DISULFID 200 200 INTERCHAIN (WITH GAMMA).
 FT DISULFID 204 204 INTERCHAIN (WITH GAMMA).
 FT DISULFID 208 293 BY SIMILARITY.
 FT DISULFID 218 247 BY SIMILARITY.
 FT DISULFID 401 414 BY SIMILARITY.
 FT CARBOHYD 371 371 N-LINKED (GLCNAC...) (PROBABLE).
 SQ SEQUENCE 468 AA; 53340 MW; 2DED42F43AA4B37 CRC64;

Query Match 84.3%; Score 43; DB 1; Length 468;
 Best Local Similarity 77.8%; Pred. No. 0.43;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HRPPLDKR 9
 Db 22 GHRPYDKK 30

RESULT 4

YEDU_ECOLI STANDARD; PRT; 231 AA.
 AC P46144; P76333; 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein yedU.
 GN YEDU OR B1962.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12; MG1655;
 RX MEDLINE=9742617; PubMed=9278503;
 RA Blaxter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.,
 RT "The complete genome sequence of Escherichia coli K-12."
 RL Science 277:1453-1474 (1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97251358; PubMed=9097040;
 RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T.,
 RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizouchi K., Mori H., Mori T., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
 RA Saito N., Sampei G., Seki Y., Sivasubraman S., Tagami H.,
 RA Takekida J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.,
 RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
 corresponding to the 40.1-50.0 min region on the linkage map."
 RL DNA Res. 3:379-392 (1996).
 RN [3]
 RP SEQUENCE OF 156-231 FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=89345179; PubMed=2527357;
 RA Hancock T., Gerwin N., Fritz H.-J.,
 RT "Nucleotide sequence of the dcm locus of Escherichia coli K12."
 RL Nucleic Acids Res. 17:5844-5844 (1989).
 RN [4]
 RP IDENTIFICATION.
 RX MEDLINE=96032851; PubMed=7567469;
 RA Borodovsky M., McIninch J., Koonin E.V., Rudd K.E., Medigue C.,
 RT "Detection of new genes in a bacterial genome using Markov models for
 three gene classes."
 RL Nucleic Acids Res. 23:3554-3562 (1995).
 CC -i- SIMILARITY: TO B.SUBTILIS YFGQ.

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DR EMBL; AE000288; AAC75028.1;
 DR EMBL; D90835; BA15790.1;
 DR EMBL; X13330; NOT_ANNOTATED_CDS.
 DR Ecocore; BG12710; yedU.
 DR InterPro; IPR002819; HD.
 DR InterPro; IPR003607; ME_Pplase_Hdc.
 DR Pfam; PF01966; HD; 1.
 DR SMART; SM00471; Hdc; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 231 AA; 25904 MW; 231A38356D16D89A CRC64;

Query Match 76.5%; Score 39; DB 1; Length 231;
 Best Local Similarity 87.5%; Pred. No. 1.3;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 HRPPLDKR 9
 Db 161 HRPPLDKR 168

RESULT 5

FIBB_RAT STANDARD; PRT; 479 AA.
 AC P1480; 01-JAN-1990 (Rel. 13, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fibrinogen beta chain precursor [Contains: Fibrinopeptide B].
 GN Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=95143385; PubMed=7841303;
 RA Courtney M.A., Bunce L.A., Neroni L.A., Simpson-Haidaris P.J.,
 RT "Cloning of the complete coding sequence of rat fibrinogen B beta
 chain cDNA: interspecies conservation of fibrin beta 15-42 primary
 structure."
 RL Blood Coagul. Fibrinolysis 5:487-496 (1994).
 RN [2]
 RP SEQUENCE OF 1-26 FROM N.A.
 RX MEDLINE=84194000; PubMed=6232608;
 RA Foxlakes D.M., Mullis N.T., Comeau C.M., Crabtree G.R.,
 RT "Potential basis for regulation of the coordinately expressed
 fibrinogen genes: homology in the 5' flanking regions."
 RL Proc. Natl. Acad. Sci. U.S.A. 81:2313-2316 (1984).
 RN [3]
 RP SEQUENCE OF 19-32.
 RA Blomback B., Blomback M., Grondahl N.J.,
 RT "Studies on fibrinopeptides from mammal."
 RL Acta Chem. Scand. 19:1789-1791 (1965).
 RN [4]
 RP SEQUENCE OF 183-479 FROM N.A.
 RX MEDLINE=89378771; PubMed=2673932;
 RA Eastman E.M., Gilula N.B.,
 RT "Cloning and characterization of a cDNA for the B beta chain of rat
 fibrinogen: evolutionary conservation of translated and
 3'-untranslated sequences."
 RL Gene 79:151-158 (1989).
 RN [5]
 RP SEQUENCE OF 425-479 FROM N.A.

```

RC STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE=87134033; PubMed=3817019;
RA Sobczak J., Lotfi A.-M., Taroux P., Duguet M.;
RT "Molecular cloning of mRNA sequences transiently induced during rat
  liver regeneration";
RL Exp. Cell Res. 169:47-56(1987).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC -----
DR EMBL; U05675; AAA64866.1; -
DR EMBL; M27220; AAA41160.1; -
DR EMBL; K01336; AAA98625.1; -
DR EMBL; M35602; AAA41159.1; -
DR PIR; A05299; A05299.
DR PIR; PE0010; PE0010.
DR HSSP; P02675; 1FZF.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Blood coagulation; Plasma; Glycoprotein; Signal.
FT SIGNAL 1 18
FT CHAIN 19 479 FIBRINOGEN BETA CHAIN.
FT PEPTIDE 19 32 FIBRINOPEPTIDE B.
FT DISULFID 211 211 INTERCHAIN (WITH THE ALPHA CHAIN)
FT (BY SIMILARITY).
FT DISULFID 215 215 INTERCHAIN (WITH THE GAMMA CHAIN)
FT (BY SIMILARITY).
FT DISULFID 219 304 BY SIMILARITY.
FT DISULFID 229 258 BY SIMILARITY.
FT DISULFID 412 425 BY SIMILARITY.
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 28 30 LSI -> ILS (IN REF. 3).
FT CONFLICT 439 439 L -> Q (IN REF. 5).
FT CONFLICT 441 441 S -> T (IN REF. 5).
FT CONFLICT 445 445 S -> A (IN REF. 5).
FT CONFLICT 467 467 R -> K (IN REF. 5).
FT CONFLICT 475 475 V -> F (IN REF. 5).
SQ SEQUENCE 479 AA; 54303 MW; EC8C6DB77C3E0ECO CRC64;

Query Match 76.5%; Score 39; DB 1; Length 479;
Best Local Similarity 55.6%; Pred. No. 2.8;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKKR 9
Db 33 GHRVDRRX 41
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DE (Fragment).
GN FGB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-13 AND 18-39.
RX MEDLINE=9182745; PubMed=2009266;
RA Weissbach L., Oddoux C., Procyk R., Grieninger G.;
RT "The beta chain of chicken fibrinogen contains an atypical thrombin
  cleavage site.";
RL Biochemistry 30:3290-3294(1991).
CC -1- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
CC CONVERTED INTO THE HARD CLOT BY FACTOR XIIIa WHICH CATALYZES THE
CC EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
CC MONOMERS.
CC -1- SIMILARITY: CONTAINS 1 FIBRINOGEN C-TERMINAL DOMAIN.
CC -----
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CC -----
DR EMBL; M58514; AAA48770.1; -
DR PIR; A38463; A38463.
DR HSSP; P02675; 1FZF.
DR InterPro; IPR002181; Fibrinogen_C.
DR Pfam; PF00147; fibrinogen_C; 1.
DR SMART; SM00186; FBG; 1.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
KW Blood coagulation; Plasma; Platelet; Glycoprotein; Sulfation.
FT NON TER 1 1
FT PEPTIDE 1 17 FIBRINOPEPTIDE B.
FT CHAIN 18 463 FIBRINOGEN BETA CHAIN.
FT MOD RES 5 5 SULFATION (BY SIMILARITY).
FT SITE 17 18 CLEAVAGE (BY THROMBIN; RELEASE
  FIBRINOPEPTIDE B).
FT DISULFID 69 69 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
FT DISULFID 80 80 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
FT DISULFID 84 84 INTERCHAIN (WITH GAMMA) (BY SIMILARITY).
FT DISULFID 197 197 INTERCHAIN (WITH ALPHA) (BY SIMILARITY).
FT DISULFID 201 201 INTERCHAIN (WITH GAMMA) (BY SIMILARITY).
FT DISULFID 205 289 BY SIMILARITY.
FT DISULFID 215 244 BY SIMILARITY.
FT DISULFID 397 410 BY SIMILARITY.
FT CARBOHYD 367 367 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 463 AA; 52678 MW; 2044CD9BA79EC7B CRC64;

Query Match 74.5%; Score 38; DB 1; Length 463;
Best Local Similarity 75.0%; Pred. No. 4.3;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPLDKKR 9
Db 19 HRPLDKRQ 26
|||||:

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RESULT 7
MRAW_ZYMMO

MRAM ZYMO STANDARD; PRT; 333 AA.
 O9RE09: O9RNM0: 41, Created)
 15-JUN-2002 (Rel. 41, Last sequence update)
 15-JUN-2002 (Rel. 41, Last annotation update)
 S-adenosyl-methyltransferase mram (EC 2.1.1.17).
 MAM OR ZM10RF5 OR ZM16ORF1.
 Zymomonas mobilis.
 Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
 Zymomonas.
 NCBI_TaxID=542;
 (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 31821 / ZM4 / CP4;
 RA Um H.W., Kang H.S.;
 RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Exhibits a S-adenosyl-dependent methyltransferase
 activity (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE MRAM FAMILY.
 CC -----
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 CC -----
 DR EMBL; AF179611; AAD53943.1; -
 DR EMBL; AF213822; AAF23786.1; -
 DR InterPro; IPR002903; Bac_Metnfrase.
 DR Pfam; PF01795; Methyltransf_5.1.
 DR ProDom; PD004685; Bac_Metnfrase; 1.
 DR TrGFams; TIGR00006; UPP0117; 1.
 DR Transferase; Methyltransferase.
 SQ SEQUENCE 333 AA; 37347 MW; A090E25F84587F79 CRC64;
 Query Match 70.6%; Score 36; DB 1; Length 333;
 Best Local Similarity 75.0%; Pred. No. 7.6;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GHRPLDKK 8
 Db 192 GHRPLDKK 199

RESULT 8
 CSEN HUMAN STANDARD; PRT; 256 AA.
 ID CSEN HUMAN STANDARD; PRT; 256 AA.
 AC O9Y2W7; O9U84; O9U85;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Calsenilin (DBE-antagonist modulator) (DBEM) (Kv channel-interacting
 protein 3) (A-type potassium channel modulatory protein 3) (KCHIP3).
 GN CSEN OR DBEM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98442695; Pubmed=9771752;
 RA Buxbaum J.D., Choi E.K., Luo Y., Lilliehook C., Crowley A.C.,
 RA Merriam D.E., Masco W.;
 RT "Calsenilin: a calcium-binding protein that interacts with the
 RT presentilin and regulates the levels of a presentilin fragment.";
 RL Nat. Med. 4:1177-1181(1998).
 (2)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Caudate;
 RX MEDLINE=99176420; Pubmed=10078534;
 RA Carrion A.M., Link W.A., Dedo F., Wellstrom B., Naranjo J.R.;

"DBEM is a Ca2+-regulated transcriptional repressor.";
 RL Nature 398:80-84(1999).
 (3)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2014034; Pubmed=10676964;
 RA An W.F., Bowley M.R., Betty M., Cao J., Ling H.-P., Mendoza G.,
 RA Hinson J.W., Mattson K.I., Strassle B.W., Trimmer J.S., Rhodes K.J.;
 RT "Modulation of A-type potassium channels by a family of calcium
 RT sensors.";
 RL Nature 403:553-556(2000).
 CC -1- FUNCTION: CALCIUM-DEPENDENT TRANSCRIPTIONAL REPRESSOR THAT BINDS
 CC TO THE DRE ELEMENT OF GENES INCLUDING PDV AND FOS. MAY PLAY A
 CC ROLE IN THE REGULATION OF PSEN2 PROTEOLYTIC PROCESSING. MODULATES
 CC K4 VOLTAGE-GATED POTASSIUM CHANNELS.
 CC -1- SUBUNIT: BINDS TO DNA AS A HOMOMULTIMER. ASSOCIATES WITH C-
 CC TERMINUS OF PSEN1 AND PSEN2. ASSOCIATES WITH KCN1.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC. ALSO MEMBRANE-BOUND. NUCLEAR
 CC (PROBABLE).
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN. WIDELY EXPRESSED AT
 CC LOWER LEVELS.
 CC -1- INDUCTION: AFFINITY FOR DNA IS REDUCED UPON BINDING TO CALCIUM.
 CC -1- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
 CC -----
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 CC -----
 DR EMBL; AF120102; AAD20350.1; -
 DR EMBL; AJ131730; CAB56836.1; -
 DR EMBL; AJ131730; CAB56835.1; -
 DR EMBL; AF199599; AAF33684.1; -
 DR HSSP; P36610; 1G8T.
 DR Genew; HGNC:15523; CSEN.
 DR MIM; 604662; -
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR001125; Recoverin.
 DR Pfam; PF00036; efhand; 3.
 DR PRINTS; PR00450; RECOVERIN.
 DR ProDom; PD000012; EF-hand; 1.
 DR SMART; SM00054; EFh; 3.
 DR PROSITE; PS00018; EF_HAND; 2.
 DR Transcription regulation; Repressor; Calcium-binding; Repeat;
 KW Nuclear protein.
 FT CA BIND 175 186 EF-HAND 1 (BY SIMILARITY)
 FT CA BIND 223 234 EF-HAND 2 (BY SIMILARITY)
 FT CONFLICT 182 182 I -> V (IN REF. 2).
 FT CONFLICT 207 207 R -> Q (IN REF. 2).
 SQ SEQUENCE 256 AA; 29231 MW; 635C3EDF8B91E1C5 CRC64;
 Query Match 66.7%; Score 34; DB 1; Length 256;
 Best Local Similarity 75.0%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GHRPLDKK 8
 Db 20 GHRPLDKK 27

RESULT 9
 CG2B-ORYSA STANDARD; PRT; 419 AA.
 ID CG2B-ORYSA STANDARD; PRT; 419 AA.
 AC O40671;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE G2/mitotic-specific cyclin 2 (B-like cyclin) (Cycos2).
 OS Oryza sativa (Rice).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoidae; Oryzaeae; Oryza.
 RT NCBI_TaxID=4530;
 RL [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Pin Gaew 53;
 RA MEDLINE=95261415; PubMed=7742859;
 RX Sauter M.; Mekheov S.L.; Kende H.;
 RT "Gibberellin promotes histone H1 kinase activity and the expression
 of cdc2 and cyclin genes during the induction of rapid growth in
 deepwater rice internodes";
 RL Plant J. 7:623-632(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Pin Gaew 53;
 RA Sauter M.;
 RT "Isolation and characterization of a cDNA encoding a mitotic cyclin of
 the CYCB2 type from rice";
 RL (In) Plant Gene Register FOR97-001.
 CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M
 (MITOSIS) TRANSITION.
 CC -1- SUBUNIT: INTERACTS WITH THE CDC2 PROTEIN KINASE TO FORM A
 SERINE/THREONINE KINASE HOLOENZYME COMPLEX ALSO KNOWN AS
 MATURATION PROMOTING FACTOR (MPF). THE CYCLIN SUBUNIT IMPARTS
 SUBSTRATE SPECIFICITY TO THE COMPLEX.
 CC -1- DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS
 ABRUPTLY DESTROYED AT MITOSIS.
 CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; X82036; CAA57556.1; -.
 DR HSSP; P30274; IVIN.
 DR InterPro; IPR004366; Cyclin.
 DR InterPro; IPR004367; Cyclin_Cterm.
 DR Pfam; PF00134; cyclin_1.
 DR Pfam; PF02984; cyclin_C_1.
 DR SMART; SM00385; CYCLIN; 2.
 DR PROSITE; PS00292; CYCLINS; 1.
 KW Cyclin; Cell cycle; Cell division; Mitosis.
 SO SEQUENCE 419 AA; 47572 MW; A8774B56BD839A5B CRC64;

Query Match 66.7%; Score 34; DB 1; Length 419;
 Best Local Similarity 62.5%; Pred. No. 25;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHRPLDK 8
 Db 64 GHRPMTK 71

RESULT 10
 VG01_HSV11
 ID_VG01_HSV11 STANDARD; PRT; 862 AA.
 AC Q00132;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DE Hypothetical gene 1 protein.
 GN 1.
 OS Ictalurid herpesvirus 1 (Channel catfish virus) (CCV).
 CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 CC Ictalurid Herpes-like viruses.
 CC NCBI_TaxID=10401;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Auburn 1;
 RX MEDLINE=92087490; PubMed=1727613;

RA Davison A.J.;
 RT "Channel catfish virus: a new type of herpesvirus";
 RL Virology 186:9-14(1992).
 CC -----
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 CC -----
 DR EMBL; M75136; AAA88182.1; -.
 DR EMBL; M75136; AAA88104.1; -.
 DR PIR; B36786; B36786.
 KW Hypothetical protein.
 SO SEQUENCE 862 AA; 93511 MW; 087E153EC71AD6 CRC64;

Query Match 66.7%; Score 34; DB 1; Length 862;
 Best Local Similarity 75.0%; Pred. No. 55;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GHRPLDK 8
 Db 768 GHRPSSK 775

RESULT 11
 CADN_RAT
 ID_CADN_RAT STANDARD; PRT; 3317 AA.
 AC P58365;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cadherin 23 precursor (Otocadherin).
 GN CDH23 OR KIA1774.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Testis;
 RX MEDLINE=2148146; PubMed=11597768;
 RA Nakajima D.; Nakayama M.; Kikuno R.; Hirosewa M.; Nagase T.; Ohara O.;
 RT "Identification of three novel non-classical cadherin genes through
 comprehensive analysis of large cDNAs";
 RL Brain Res. Mol. Brain Res. 94:85-95(2001).
 CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 They preferentially interact with themselves in a homophilic
 manner in connecting cells. Cadherin 23 may function as hair
 bundle organizer perhaps by cross-linking the stereocilia (By
 similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 27 cadherin domains.
 CC -----
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 CC -----
 DR EMBL; AB053447; BAB61904.1; -.
 DR InterPro; IPR002126; Cadherin.
 DR Pfam; PF00028; cadherin; 27.
 DR SMART; SM00112; CA; 26.
 DR PROSITE; PS00232; CADHERIN_1; 17.
 DR PROSITE; PS50268; CADHERIN_2; 27.
 KW Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
 KW Signal; Multigene family.
 FT SIGNAL 1 POTENTIAL. 23

FT	CHAIN	24	3317	CADHERIN 23.
FT	DOMAIN	24	3062	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	3063	3083	POTENTIAL.
FT	DOMAIN	3084	3317	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	3317	132	CADHERIN 1.
FT	DOMAIN	133	236	CADHERIN 2.
FT	DOMAIN	237	348	CADHERIN 3.
FT	DOMAIN	349	458	CADHERIN 4.
FT	DOMAIN	459	559	CADHERIN 5.
FT	DOMAIN	560	669	CADHERIN 6.
FT	DOMAIN	670	782	CADHERIN 7.
FT	DOMAIN	777	888	CADHERIN 8.
FT	DOMAIN	889	993	CADHERIN 9.
FT	DOMAIN	994	1100	CADHERIN 10.
FT	DOMAIN	1101	1206	CADHERIN 11.
FT	DOMAIN	1208	1311	CADHERIN 12.
FT	DOMAIN	1312	1416	CADHERIN 13.
FT	DOMAIN	1418	1525	CADHERIN 14.
FT	DOMAIN	1527	1632	CADHERIN 15.
FT	DOMAIN	1633	1742	CADHERIN 16.
FT	DOMAIN	1743	1849	CADHERIN 17.
FT	DOMAIN	1850	1957	CADHERIN 18.
FT	DOMAIN	1958	2067	CADHERIN 19.
FT	DOMAIN	2068	2172	CADHERIN 20.
FT	DOMAIN	2173	2291	CADHERIN 21.
FT	DOMAIN	2295	2400	CADHERIN 22.
FT	DOMAIN	2508	2597	CADHERIN 23.
FT	DOMAIN	2609	2699	CADHERIN 24.
FT	DOMAIN	2720	2720	CADHERIN 25.
FT	DOMAIN	2727	2844	CADHERIN 26.
FT	DOMAIN	2845	2973	CADHERIN 27.
FT	CARBOHYD	155	155	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	206	206	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	349	349	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	391	391	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	432	432	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	464	464	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	470	470	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	600	600	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	692	692	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	763	763	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	808	808	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	825	825	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	939	939	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	999	999	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1016	1016	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1169	1169	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1280	1280	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1313	1313	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1471	1471	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1532	1532	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1649	1649	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1665	1665	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1816	1816	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1855	1855	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1887	1887	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	1900	1900	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	2012	2012	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	2048	2048	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	2127	2127	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	2166	2166	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	2193	2193	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	2261	2261	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	2355	2355	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	2367	2367	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	2576	2576	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	2614	2614	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	2747	2747	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	2806	2806	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	2875	2875	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	2894	2894	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	2939	2939	N-LINKED (GLCNAC. . .)
FT	CARBOHYD	2979	2979	N-LINKED (GLCNAC. . .)

SO SEQUENCE 3317 AA; 365448 MW; CEF397A066BF0986 CRC64;
 Query Match 66.7%; Score 34; DB 1; Length 3317;
 Best Local Similarity 66.7%; Pred. No. 2.4e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHRPLDKR 9
 Db 1160 GHRPLDKR 1168

RESULT 12
 ID CADN HUMAN STANDARD; PRT; 3354 AA.
 AC 09H251; 09H493;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Cadherin 23 precursor (Otocadherin).
 GN CDH23 OR KIA11774.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, VARIANTS USH1D M-1281 DEL;
 RP H-1496 AND Q-1746, AND VARIANTS C-3; A-490; N-496; T-1222; C-1349;
 RP N-1351; A-1575; I-1671; I-1675; Q-1804; S-1999; K-2044; Q-2358;
 RP L-2380; Q-2588 AND L-3125.
 RX MEDLINE=20578759; PubMed=1138009;
 RA Boltz H., Von Bredelow B., Ramirez A., Bryda E.C., Kutsche K.,
 RA Nothwang H.G., Seeliger M., Del C.-Salcedo Cabrera M.,
 RA Villa Caballero M., Pelaez Molina O., Gal A., Kubisch C.;
 RT "Mutation of CDH23, encoding a new member of the cadherin gene family,
 RT Nat. Genet. 27:108-112(2001)."
 RN [2]
 RP SEQUENCE OF 803-3354 FROM N.A., ALTERNATIVE SPLICING, AND VARIANTS
 RP DPNB12 N-990; N-2045; N-2202; N-2950; C-2956 AND T-3059.
 RX PubMed=11090341;
 RA Bork J.M., Peters L.M., Riazuddin S., Bernstein S.L., Ahmed Z.M.,
 RA Ness S.L., Polomeno R., Ramesh A., Schloss M., Srisaibpathy C.R.S.,
 RA Wayne S., Bellman S., Desmukh D., Ahmed Z., Khan S.N.,
 RA Kaloustian V.M.D., Li X.C., Jalwani A., Riazuddin S.,
 RA Bitner-Glindzicz M., Nance W.E., Liu X.-Z., Wistow G., Smith R.J.H.,
 RA "usher syndrome ID and nonsyndromic autosomal recessive deafness
 RT DPNB12 are caused by allelic mutations of the novel cadherin-like
 RT gene CDH23.";
 RL Am. J. Hum. Genet. 68:26-37(2001).
 RN [3]
 RP SEQUENCE OF 2173-3354 FROM N.A. (ISOFORM 4).
 RP TISSUE=Brain;
 RX MEDLINE=21481446; PubMed=11597768;
 RA Nakajima D., Nakayama M., Kikuno R., Hirosewa M., Nagase T., Ohara O.;
 RT "Identification of three novel non-classical cadherin genes through
 RT comprehensive analysis of large cDNAs.";
 RL Brain Res. Mol. Brain Res. 94:85-95(2001).
 RN [4]
 RP FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
 RP They preferentially interact with themselves in a homophilic
 RP manner in connecting cells. Cadherin 23 may function as hair
 RP bundle organizer perhaps by cross-linking the stereocilia (by
 RP similarity).
 RP SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 RP ALTERNATIVE PRODUCTS: At least 4 isoforms; 1 (shown here), 2, 3
 RP and 4; are produced by alternative splicing.
 RP TISSUE SPECIFICITY: Particularly strong expression in the retina.
 RP Found also in the cochlea.
 RP DISRASE: Defects in CDH23 are the cause of Usher syndrome type 1D
 RP (USH1D). Usher syndrome type 1 is an autosomal recessive disorder
 RP characterized by congenital profound sensorineural hearing loss,
 RP constant vestibular dysfunction and prepubertal onset of retinitis
 RP pigmentosa leading to blindness. Usher syndrome is the most common

CC cause of combined deafness and blindness in developed countries.
 CC -1- DISEASE: Defects in CDH23 are the cause of a form of nonsyndromic
 CC autosomal recessive deafness (DFNB12).
 CC -1- SIMILARITY: Contains 27 cadherin domains.
 CC -----
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 CC -----
 CC DR EMBL; AF312024; AAG48303.1; -
 CC DR EMBL; AY010111; AAG27034.2; -
 CC DR EMBL; AB053445; BAB61902.1; -
 CC DR HSSP; P15116; INCU.
 CC DR Gene; HGNC:13733; CDH23.
 CC DR MIM; 60516; -
 CC DR MIM; 601067; -
 CC DR MIM; 601386; -
 CC DR InterPro; IPR002126; Cadherin.
 CC DR Pfam; PF00028; Cadherin.
 CC DR PRINTS; PRO0205; CADHERIN.
 CC DR SMART; SM00112; CA; 26.
 CC DR PROSITE; PS00232; CADHERIN_1; 17.
 CC DR PROSITE; PS0268; CADHERIN_2; 27.
 CC KW Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
 CC Signal; Multigene family; Alternative splicing; Vision; Polymorphism;
 CC Disease mutation; Usher syndrome; Deafness; Retinitis pigmentosa.
 CC FT SIGNAL 1 23
 CC FT CHAIN 24 3354
 CC FT DOMAIN 24 3064 EXTRACELLULAR (POTENTIAL).
 CC FT TRANSMEM 3065 3354 POTENTIAL.
 CC FT DOMAIN 34 132 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 133 236 CADHERIN 1.
 CC FT DOMAIN 237 348 CADHERIN 2.
 CC FT DOMAIN 349 460 CADHERIN 3.
 CC FT DOMAIN 461 561 CADHERIN 4.
 CC FT DOMAIN 562 671 CADHERIN 5.
 CC FT DOMAIN 672 784 CADHERIN 6.
 CC FT DOMAIN 785 890 CADHERIN 7.
 CC FT DOMAIN 891 995 CADHERIN 8.
 CC FT DOMAIN 996 1102 CADHERIN 9.
 CC FT DOMAIN 1103 1208 CADHERIN 10.
 CC FT DOMAIN 1210 1313 CADHERIN 11.
 CC FT DOMAIN 1314 1418 CADHERIN 12.
 CC FT DOMAIN 1420 1527 CADHERIN 13.
 CC FT DOMAIN 1529 1634 CADHERIN 14.
 CC FT DOMAIN 1635 1744 CADHERIN 15.
 CC FT DOMAIN 1745 1851 CADHERIN 16.
 CC FT DOMAIN 1852 1959 CADHERIN 17.
 CC FT DOMAIN 1960 2069 CADHERIN 18.
 CC FT DOMAIN 2070 2174 CADHERIN 19.
 CC FT DOMAIN 2175 2293 CADHERIN 20.
 CC FT DOMAIN 2297 2402 CADHERIN 21.
 CC FT DOMAIN 2403 2509 CADHERIN 22.
 CC FT DOMAIN 2510 2611 CADHERIN 23.
 CC FT DOMAIN 2612 2722 CADHERIN 24.
 CC FT DOMAIN 2729 2846 CADHERIN 25.
 CC FT DOMAIN 2847 2975 CADHERIN 26.
 CC FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 349 349 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 393 393 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 434 434 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 466 466 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 472 472 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 652 652 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 694 694 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 765 765 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 810 810 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 827 827 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 941 941 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1001 1001 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1018 1018 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1171 1171 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1282 1282 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1315 1315 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1473 1473 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1534 1534 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1651 1651 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1667 1667 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1818 1818 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1857 1857 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1889 1889 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1902 1902 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2013 2013 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2050 2050 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2129 2129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2168 2168 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2195 2195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2263 2263 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2357 2357 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2369 2369 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2616 2616 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2749 2749 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2808 2808 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2877 2877 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2896 2896 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2941 2941 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 2981 2981 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPPLIC 379 380 MISSING (IN ISOFORM 3).
 FT VARSPPLIC 1403 1403 MISSING (IN ISOFORM 3).
 FT VARSPPLIC 3212 3246 MISSING (IN ISOFORM 4).
 FT VARIANT 3 3 R -> C
 FT VARIANT 490 490 /FTId=VAR_012166.
 FT VARIANT 496 496 G -> A.
 FT VARIANT 496 496 /FTId=VAR_012167.
 FT VARIANT 990 990 S -> N.
 FT VARIANT 990 990 /FTId=VAR_012168.
 FT VARIANT 1222 1222 D -> N (IN DFNB12).
 FT VARIANT 1222 1222 /FTId=VAR_012169.
 FT VARIANT 1281 1281 A -> T.
 FT VARIANT 1281 1281 /FTId=VAR_012170.
 FT VARIANT 1349 1349 MISSING (IN USH1D).
 FT VARIANT 1349 1349 /FTId=VAR_012171.
 FT VARIANT 1351 1351 R -> C.
 FT VARIANT 1351 1351 /FTId=VAR_012172.
 FT VARIANT 1496 1496 D -> N.
 FT VARIANT 1496 1496 /FTId=VAR_012173.
 FT VARIANT 1575 1575 O -> H (IN USH1D).
 FT VARIANT 1575 1575 /FTId=VAR_012174.
 FT VARIANT 1671 1671 T -> A.
 FT VARIANT 1671 1671 /FTId=VAR_012175.
 FT VARIANT 1671 1671 T -> S.
 FT VARIANT 1675 1675 /FTId=VAR_012176.
 FT VARIANT 1746 1746 V -> I.
 FT VARIANT 1746 1746 /FTId=VAR_012177.
 FT VARIANT 1804 1804 R -> Q (IN USH1D; MLUD RETINAL AFFECTON).
 FT VARIANT 1804 1804 /FTId=VAR_012178.
 FT VARIANT 1999 1999 R -> Q.
 FT VARIANT 1999 1999 /FTId=VAR_012179.
 FT VARIANT 2044 2044 T -> S.
 FT VARIANT 2044 2044 /FTId=VAR_012180.
 FT VARIANT 2045 2045 E -> K.
 FT VARIANT 2045 2045 /FTId=VAR_012181.
 FT VARIANT 2045 2045 D -> N (IN DFNB12).
 Query Match 66.7%; Score 34; DB 1; Length 3354;
 Best Local Similarity 66.7%; Pred. No. 2;4e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 1 GHRPLDKR 9

Db 1162 GPRLEDR 1170

RESULT 13
ID CADN MOUSE STANDARD: PRT: 3354 AA.
AC O99PF4; O99NH1; O9D4N9;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Cadherin 23 precursor (Otocadherin).
GN Cdh23.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RP (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA MEDLINE=20578758; PubMed=1138008;
RA Di Palma F., Holme R.H., Bryda E.C., Belyantseva I.A., Pellegrino R.,
RA Kachar B., Steel K.P., Noben-Trauth K.,
RA "Mutations in Cdh23, encoding a new type of cadherin, cause
RA stereocilia disorganization in waltzer, the mouse model for Usher
RA syndrome type II.";
RA Nat. Genet. 27:103-107(2001).
RN (2)
RN SEQUENCE FROM N.A. (ISOFORM 2).
RP TISSUE=Brain;
RX MEDLINE=21280917; PubMed=11386759;
RA Wilson S.M., Householder D.B., Coppola V., Tessarollo L., Fritzsche B.,
RA Lee E.-C., Goss D., Carlson G.A., Copeland N.G., Jenkins N.A.,
RA "Mutations in Cdh23 cause nonsyndromic hearing loss in waltzer mice.";
RA Genomics 74:228-233(2001).
RN (3)
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein W.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzaletti U., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszewski A., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
RA Hayashizaki Y.,
RA "Functional annotation of a full-length mouse cDNA collection.";
RA Nature 409:685-690(2001).
RN (4)
RN SEQUENCE FROM N.A.
RA Fu Y., Wang O., Roe B.A.,
RA Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN (5)
RN GENOMIC ORGANIZATION, ALTERNATIVE SPLICING, VARIANT WALTZER
RP 2718-ASN-GLU-PRO-2720 DEL, AND VARIANTS PRO-5; VAL-229; LYS-891;
RP ILE-1137; ARG-1236; VAL-2025; VAL-2026; THR-2217; HIS-2222; ARG-2270
RP AND ALA-2617.
RX MEDLINE=21623040; PubMed=11750125;
RA Di Palma F., Pellegrino R., Noben-Trauth K.,
RA "Genomic structure, alternative splice forms and normal and mutant
RA alleles of cadherin 23 (Cdh23).";
RA Gene 281:31-41(2001).

CC -1- FUNCTION: Cadherins are calcium dependent cell adhesion proteins.
CC They preferentially interact with themselves in a homophilic
CC manner in connecting cells. Cadherin 23 may function as hair
CC bundle organizer perhaps by cross-linking the stereocilia.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: In adult animals relatively high levels of
CC expression are found in testis, skeletal muscle, heart, eye and
CC thymus, and lower expression in kidney, lung and brain. Found in
CC the sensory hair cells of the inner ear.
CC -1- DISEASE: Defects in Cdh23 are the cause of waltzer (v) phenotype.
CC waltzer mice are characterized by deafness and vestibular
CC dysfunction due to degeneration of the neuroepithelium within the
CC inner ear.
CC -1- SIMILARITY: Contains 27 cadherin domains.
CC -----
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CC -----
DR EMBL; AF308939; AAC52817.1; -;
DR EMBL; AY026062; AAK07670.1; -;
DR EMBL; AK016365; BAB30206.1; ALT SEQ.
DR EMBL; AC079818; -; NOT_ANNOTATED_CDS.
DR EMBL; AC079819; -; NOT_ANNOTATED_CDS.
DR EMBL; AC079082; -; NOT_ANNOTATED_CDS.
DR HSSP; P15116; INCU.
DR MGI; MGI:1890219; Cdh23.
DR InterPro; IPR002126; Cadherin.
DR Pfam; PF00028; cadherin; 51.
DR PRINTS; PR00205; CADHERIN.
DR SMART; SM00112; CA; 26.
DR PROSITE; PS00232; CADHERIN_1; 17.
DR PROSITE; PS0268; CADHERIN_2; 27.
KW Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Repeat;
KW Signal; Multigene family; Alternative splicing; Deafness;
KW Polymorphism; Disease mutation.
FT CHAIN 1 23
FT DOMAIN 24 3354 CADHERIN 23.
FT TRANSMEM 3065 3085 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 3086 3354 POTENTIAL.
FT DOMAIN 133 132 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 237 348 CADHERIN 1.
FT DOMAIN 349 460 CADHERIN 2.
FT DOMAIN 461 561 CADHERIN 3.
FT DOMAIN 562 671 CADHERIN 4.
FT DOMAIN 672 784 CADHERIN 5.
FT DOMAIN 779 890 CADHERIN 6.
FT DOMAIN 891 995 CADHERIN 7.
FT DOMAIN 996 1102 CADHERIN 8.
FT DOMAIN 1103 1208 CADHERIN 9.
FT DOMAIN 1210 1313 CADHERIN 10.
FT DOMAIN 1314 1418 CADHERIN 11.
FT DOMAIN 1420 1527 CADHERIN 12.
FT DOMAIN 1529 1634 CADHERIN 13.
FT DOMAIN 1635 1744 CADHERIN 14.
FT DOMAIN 1745 1851 CADHERIN 15.
FT DOMAIN 1852 1959 CADHERIN 16.
FT DOMAIN 1960 2069 CADHERIN 17.
FT DOMAIN 2070 2174 CADHERIN 18.
FT DOMAIN 2175 2293 CADHERIN 19.
FT DOMAIN 2297 2402 CADHERIN 20.
FT DOMAIN 2403 2509 CADHERIN 21.
FT DOMAIN 2510 2611 CADHERIN 22.
FT DOMAIN 2614 2722 CADHERIN 23.
FT DOMAIN 2729 2846 CADHERIN 24.
FT CADHERIN 25.
FT CADHERIN 26.

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FT DOMAIN 2847 2975
FT CARBOHYD 155 155
FT CARBOHYD 206 206
FT CARBOHYD 349 349
FT CARBOHYD 393 393
FT CARBOHYD 434 434
FT CARBOHYD 466 466
FT CARBOHYD 472 472
FT CARBOHYD 602 602
FT CARBOHYD 694 694
FT CARBOHYD 765 765
FT CARBOHYD 810 810
FT CARBOHYD 827 827
FT CARBOHYD 941 941
FT CARBOHYD 1001 1001
FT CARBOHYD 1018 1018
FT CARBOHYD 1171 1171
FT CARBOHYD 1282 1282
FT CARBOHYD 1315 1315
FT CARBOHYD 1473 1473
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FT CARBOHYD 1667 1667
FT CARBOHYD 1818 1818
FT CARBOHYD 1857 1857
FT CARBOHYD 1889 1889
FT CARBOHYD 1902 1902
FT CARBOHYD 2014 2014
FT CARBOHYD 2050 2050
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FT CARBOHYD 2168 2168
FT CARBOHYD 2195 2195
FT CARBOHYD 2263 2263
FT CARBOHYD 2357 2357
FT CARBOHYD 2369 2369
FT CARBOHYD 2578 2578
FT CARBOHYD 2616 2616
FT CARBOHYD 2749 2749
FT CARBOHYD 2808 2808
FT CARBOHYD 2877 2877
FT CARBOHYD 2896 2896
FT CARBOHYD 2941 2941
FT CARBOHYD 2981 2981
FT VASPLIC 3212 3246
FT VARIANT 5 5
FT VARIANT 229 229
FT VARIANT 891 891
FT VARIANT 1137 1137
FT VARIANT 1236 1236
FT VARIANT 2025 2025
FT VARIANT 2026 2026
FT VARIANT 2217 2217
FT VARIANT 2222 2222
FT VARIANT 2270 2270
FT VARIANT 2617 2617
FT VARIANT 2718 2720
FT CONFLICT 94 94
FT CONFLICT 142 143
FT CONFLICT 248 251
FT CONFLICT 3262 3262

Query Match Similarity 66.7%; Score 34; DB 1; Length 3354;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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AC Q9RMW2;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein PXO2-72.
GN PXO2-72.
OS Bacillus anthracis.
OG Plasmid PXO2.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RA Okinaka R.T., Clout K., Hampton O., Hill K.K., Keim P., Lamke G.,
RA Kurnano S., Menter D., Martinez Y., Svensson R., Tatum L.R.,
RA Brown A.E., Jackson P.J.
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AF188935; AAF13677.1; -
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 81 AA; 9732 MW; 140A366C200228AD CRC64;

Query Match Similarity 64.7%; Score 33; DB 1; Length 81;
Best Local Similarity 62.5%; Pred. No. 6.6;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 2 HRPDKKR 9
50 YRPLEKKR 57

RESULT 15
YF33 YEAST STANDARD; PRT; 155 AA.
ID YF33 YEAST
AC P43587;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Hypothetical 18.2 kDa protein in NIT96-MPRI intergenic region.
GN YFR003C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=5288C / AB972;
RX MEDLINE=95400292; Pubmed=7670463;
RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
RA Sasanuma S.-I., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,
RA Yamazaki M., Tashiro H., Eki T.;
RT "Analysis of the nucleotide sequence of chromosome VI from
RT Saccharomyces cerevisiae."
RL Nat. Genet. 10:261-268(1995).
RL
CC -----
CC -I- SIMILARITY: TO S. POMBE SPAC6B12.13.
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CC -----
DR EMBL; D50617; BAA09242.1; -
DR SGD; S0001899; YFR003C.

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KW Hypothetical protein.
FT DOMAIN 93 103 POLY-SER.
SQ SEQUENCE 155 AA; 18187 MW; E191B4DCDSEF8A1 CRC64;
Query Match 64.7%; Score 33; DB 1; Length 155;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 HRPIDKKR 9
|||:||||
Db 123 HRKLEKKR 130

Search completed: June 27, 2003, 17:17:09
Job time : 7.3 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 17:14:41 ; Search time 21.6 Seconds

(without alignments)
85.853 Million cell updates/sec

Title: US-10-019-439-2

Perfect score: 51

Sequence: 1 GHRPLDKKR 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_protent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	51	100.0	411 4 Q8WM77	Q8WM77 homo sapien
2	39	76.5	231 16 Q8XB89	Q8XB89 escherichia
3	39	76.5	673 3 Q94271	Q94271 schizosacch
4	39	76.5	959 2 Q46583	Q46583 desulfocib
5	38	74.5	244 2 Q93JUS	Q93JUS pseudomonas
6	37	72.5	275 10 Q43476	Q43476 hordeum vul
7	37	72.5	474 5 Q95RFO	Q95RFO dirosophila
8	37	72.5	474 5 Q9VMQ6	Q9VMQ6 dirosophila
9	37	72.5	474 5 Q9VMQ3	Q9VMQ3 dirosophila
10	36	70.6	923 5 Q9VA50	Q9VA50 dirosophila
11	36	70.6	195 16 Q930R0	Q930R0 rhizobium m
12	36	70.6	201 16 Q92XY9	Q92XY9 rhizobium m
13	36	70.6	471 10 Q8SBA0	Q8SBA0 oryza sativ
14	36	70.6	505 4 Q9HA50	Q9HA50 homo sapien
15	36	70.6	694 16 Q8VUW0	Q8VUW0 mycobacteri
16	36	70.6	735 10 Q94EB7	Q94EB7 oryza sativ

17	36	70.6	1371 4 Q9Y2K2	Q9Y2K2 homo sapien
18	36	70.6	1490 10 Q9M1C7	Q9M1C7 arabidopsis
19	35	68.6	225 3 Q74112	Q74112 neurospora
20	35	68.6	225 16 Q9RXW3	Q9RXW3 deinococcus
21	35	68.6	271 2 Q9MWE0	Q9MWE0 agrobacteri
22	35	68.6	334 16 Q92P01	Q92P01 rhizobium m
23	35	68.6	368 16 Q9KXQ8	Q9KXQ8 streptomyce
24	35	68.6	433 10 Q9M7J5	Q9M7J5 lophopyrum
25	35	68.6	571 16 Q8UKH9	Q8UKH9 agrobacteri
26	35	68.6	820 10 Q9FY05	Q9FY05 populus tre
27	34	66.7	151 2 P71490	P71490 methylovicr
28	34	66.7	234 4 Q96T40	Q96T40 homo sapien
29	34	66.7	358 5 Q9VAJ1	Q9VAJ1 dirosophila
30	34	66.7	402 16 Q8U1H0	Q8U1H0 agrobacteri
31	34	66.7	417 16 Q8R9G7	Q8R9G7 thermoaer
32	34	66.7	432 12 Q9OH50	Q9OH50 gallid hep
33	34	66.7	434 17 Q9XG11	Q9XG11 lycopersico
34	34	66.7	480 17 Q9V022	Q9V022 pyrococcus
35	34	66.7	554 10 P93719	P93719 petunia hyb
36	34	66.7	585 3 P78978	P78978 yarowia li
37	34	66.7	735 10 Q93ZU3	Q93ZU3 arabidopsis
38	34	66.7	735 10 Q82754	Q82754 arabidopsis
39	34	66.7	795 10 Q9S1Z7	Q9S1Z7 arabidopsis
40	34	66.7	830 16 Q8XR09	Q8XR09 ralsconia s
41	33	64.7	67 9 Q94MW0	Q94MW0 bacterioph
42	33	64.7	162 3 Q08230	Q08230 saccharomyc
43	33	64.7	226 16 Q983T8	Q983T8 rhizobium l
44	33	64.7	250 4 Q9NSV7	Q9NSV7 homo sapien
45	33	64.7	266 2 Q9ZFL2	Q9ZFL2 bacillus st

ALIGNMENTS

RESULT 1	Q8WM77	PRELIMINARY;	PRT;	411 AA.
ID	Q8WM77			
AC	Q8WM77			
DT	01-MAR-2002 (TREMBLrel. 20, Created)			
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Hypothetical 46.9 KDa protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
RA	Strausberg R.;			
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC020762; AAH20762.1; -			
DR	InterPro; IPR002181; Fibrinogen_C.			
DR	InterPro; IPR001019; Grotein_alpha.			
DR	Pfam; PF00147; Fibrinogen_C; 1.			
DR	Pfam; PF00503; G-alpha; 1.			
DR	SMART; SM00186; FBG; 1.			
DR	SMART; SM00275; G-alpha; 1.			
RW	Hypothetical protein.			
SO	SEQUENCE 411 AA; 46884 MW; 601E4EA47F60E056 CRC64;			
Query Match	Score 51; DB 4; Length 411;			
Best Local Similarity	100.0%; Pred. No. 0.055;			
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 GHRPLDKKR 9			
DB	45 GHRPLDKKR 53			
RESULT 2	Q8XB89	PRELIMINARY;	PRT;	231 AA.
ID	Q8XB89			

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AC O8XB89;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Olf, hypothetical protein.
GN YBDJ OR Z3055 OR ECS2700.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / BDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobleck E.J., Davis N.W., Lim A., Dimalanta E.T., Potomousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
RA Kihara S., Shiba T., Hattori M., Shingawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
DR EMBL; AE005418; AAG56976.1; -
DR EMBL; AP002559; BAB36123.1; -
DR InterPro: IPR002819; HD.
DR InterPro: IPR003607; ME_Ppase_HDC.
DR Pfam; PF01966; HD; 1.
DR SMART; SM00471; HDC; 1.
KW Complete proteome.
SQ SEQUENCE 231 AA; 25835 MW; 34D81C1ADAB83682 CRC64;

Query Match
Best Local Similarity 76.5%; Score 39; DB 16; Length 231;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPDLKKR 9
DB 161 HRPDLKKR 168

RESULT 3
O94271 PRELIMINARY; PRT; 673 AA.
AC O94271;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Zinc finger protein.
GN SPBP887.23.
OS Schizosaccharomyces pombe (Fission Yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA Beck A., Reinhardt R., Lyne M., Rajandream M.A., Barrell B.G.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL032684; CAA21808.1; -
DR InterPro; IPR001841; Znf_ring.
DR SMART; SM00184; RING; 1.

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DR PROSITE; PS00518; ZF_RING_1; 1.
KW Zinc-finger.
SQ SEQUENCE 673 AA; 76459 MW; 7317BDAD768FC883 CRC64;

Query Match
Best Local Similarity 76.5%; Score 39; DB 3; Length 673;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDKKR 9
DB 160 GHRPLDKKR 168

RESULT 4
O46583 PRELIMINARY; PRT; 959 AA.
AC O46583;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE DCRH.
GN DCRH.
OS Desulfovibrio vulgaris (strain Hildenborough).
OC Bacteria; Proteobacteria; delta subdivision; Desulfovibrionaceae;
OC Desulfovibrio.
OX NCBI_TaxID=882;
RN [1]
RP SEQUENCE OF 605-727 FROM N.A.
RC STRAIN=HILDENBOROUGH;
RX MEDLINE=94117369; PubMed=8288529;
RA Deckers H.M., Voordouw G.;
RT "Identification of a large family of genes for putative chemoreceptor
RT proteins in an ordered library of the Desulfovibrio vulgaris
RT Hildenborough genome.";
RL J. Bacteriol. 176:351-358(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=HILDENBOROUGH;
RX MEDLINE=96433451; PubMed=8836438;
RA Deckers H.M., Voordouw G.;
RT "The dcr gene family of Desulfovibrio: implications from the sequence
RT of dcrH and phylogenetic comparison with other mcp genes.";
RL Antonie Van Leeuwenhoek 70:21-29(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=HILDENBOROUGH;
RA Voordouw G.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U30319; AAB50497.1; -
DR HSSP; P02942; 10U7;
DR InterPro: IPR004089; Chmtaxis_transd.
DR InterPro: IPR003660; HAMP.
DR InterPro: IPR002063; Hemerythrin.
DR Pfam; PF00672; HAMP; 1.
DR Pfam; PF01814; Hemerythrin; 1.
DR Pfam; PF00015; MCPsignal; 1.
DR ProDom; PD006099; Hemerythrin; 1.
DR SMART; SM00304; HAMP; 1.
DR SMART; SM00283; MA; 1.
SQ SEQUENCE 959 AA; 104729 MW; 45050E840954D42 CRC64;

Query Match
Best Local Similarity 76.5%; Score 39; DB 2; Length 959;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPDLKKR 9
DB 513 HRPDLKKR 520

RESULT 5
O93JUS PRELIMINARY; PRT; 244 AA.
ID O93JUS

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AC Q93JUS;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 27.9 kDa protein.
OS Pseudomonas stutzeri A15.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=91504;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHINA.
RA Desnoues N., Lin M., Elmerich C.;
RT "Organisation of nit genes in Pseudomonas stutzeri A15, a rice
  endophyte.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ133205; CAC42170.1; -.
DR InterPro; IPR004830; LRV.
DR Pfam; PF01816; LRV; 5.
DR ProDom; PD038723; Unk_DeinSyn; 1.
KM Hypothetical protein.
SQ SEQUENCE 244 AA; 27906 MW; A983A2BD7AA9A367 CRC64;

Query Match 74.5%; Score 38; DB 2; Length 244;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKK 8
Db 180 GHRPLNRK 187

RESULT 6
Q43476 PRELIMINARY; PRT; 275 AA.
ID Q43476;
AC Q43476;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Mammalian acyl CoA oxidase homologous (Fragment).
GN CDR29.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ARDA. TISSUE=GREEN LEAF;
RA Grossi M., Gulli M., Spanca A.M., Cattivelli L.;
RT "Characterization of two barley genes that respond rapidly to
  dehydration stress.";
RL Plant Sci. 105:71-80(1995).
DR EMBL; X84055; CAA58874.1; -.
DR InterPro; IPR001552; ACYL_COA_dh.
DR InterPro; IPR005202; GRAS.
DR Pfam; PF00441; ACYL_COA_dh; 1.
DR Pfam; PF03514; GRAS; 1.
FT NON_TER 1
SQ SEQUENCE 275 AA; 30689 MW; 332811FD05827472 CRC64;

Query Match 72.5%; Score 37; DB 10; Length 275;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDKK 9
Db 225 GHRPLNRK 233

RESULT 7
Q95RFO PRELIMINARY; PRT; 474 AA.
ID Q95RFO;
AC Q95RFO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Drosophila melanogaster (fruit fly).
GN CG6961.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
  Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
  Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
  Munoz J., Pacled J., Paragas V., Park S., Phouanavong S., Wan K.,
  Yu C., Lewis S.E., Rubin G.M., Celniker S.;
  Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY061430; AAL28978.1; -.
DR FlyBase; FBgn0030959; CG6961.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR01656; VACCYTOTOXIN.
DR PROSITE; PSS0102; RRM; 1.
SQ SEQUENCE 474 AA; 53015 MW; 44C8C8DA263899B4 CRC64;

Query Match 72.5%; Score 37; DB 5; Length 474;
Best Local Similarity 75.0%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYRPLDKK 8
Db 19 GYRPLDKK 26

RESULT 8
Q9VMQ6 PRELIMINARY; PRT; 474 AA.
ID Q9VMQ6;
AC Q9VMQ6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CG18259 protein.
GN CG18259.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; Pubmed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
  Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
  George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
  Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
  Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
  Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
  Abril J.F., Agbayani A., An H.-J., Andrews-Franko C., Baldwin D.,
  Ballew R.W., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
  Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
  Borokan D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
  Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
  Cherry J.M., Cawley S., Dahlke C., Daventport L.B., Davies P.,
  de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
  Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
  Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
  Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
  Glodet A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Kaipen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Munkulov G., Mlshina N.V., Mobarly C., Morris J., Mostreft A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Zhong X.H., Zhong F.N., Zhong W., Zhou X., Zhang G., Zhao Q., Zheng L.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 DR EMBL: AEO03510; AAF48882.1; -
 DR HSSP: P11940; 1CVJ.
 DR FLYBASE: FBgn0030956; CG18259.
 DR InterPro: IPR000504; RNA_rec_mct.
 DR Pfam: PF00076; rrm; 1.
 DR PRINTS: PR01656; VACCYTOTOXIN.
 DR SMART: SM00360; RRM; 1.
 DR PROSITE: PSS0102; RRM; 1.
 SQ SEQUENCE 474 AA; 52999 MW; E08C3FBIAB29C1E CRC64;

Query Match
 Best Local Similarity 72.5%; Score 37; DB 5; Length 474;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPDKK 8
 Db 19 GYRPLDKK 26

RESULT 9
 Q9VW03 PRELIMINARY; PRT; 474 AA.
 ID Q9VW03
 AC Q9VW03
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE CG6961 protein.
 GN CG6961.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,

RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Kaipen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Munkulov G., Mlshina N.V., Mobarly C., Morris J., Mostreft A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Zhong X.H., Zhong F.N., Zhong W., Zhou X., Zhang G., Zhao Q., Zheng L.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 DR EMBL: AEO03510; AAF48885.1; -
 DR HSSP: P11940; 1CVJ.
 DR FLYBASE: FBgn0030959; CG6961.
 DR InterPro: IPR000504; RNA_rec_mct.
 DR Pfam: PF00076; rrm; 1.
 DR PRINTS: PR01656; VACCYTOTOXIN.
 DR SMART: SM00360; RRM; 1.
 DR PROSITE: PSS0102; RRM; 1.
 SQ SEQUENCE 474 AA; 53001 MW; E3555F1C72BD1DA CRC64;

Query Match
 Best Local Similarity 72.5%; Score 37; DB 5; Length 474;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPDKK 8
 Db 19 GYRPLDKK 26

RESULT 10
 Q9VA50 PRELIMINARY; PRT; 923 AA.
 ID Q9VA50
 AC Q9VA50
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE CG9713 protein.
 GN CG9713.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glaeser K.,
 RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laeko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Maitel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mlehnha N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusekern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Renner C., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spreading A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhou X., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*,"
 RL Science 287:2185-2195(2000).
 DR EMBL; AB003774; AAF57073.1; -
 DR Flybase; FBgn0039793; CG9713.
 DR InterPro; IPR005123; 2OG-Fell_Oxy.
 DR Pfam; PF01171; 2OG-Fell_Oxy; 2.
 SQ SEQUENCE 923 AA; 105446 MW; 7E4A5D9B8E0C929 CRC64;

Query Match 72.5%; Score 37; DB 5; Length 923;
 Best Local Similarity 85.7%; Pred. No. 77;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHRPLDK 7
 |||||
 Db 539 GHRPLEK 545

RESULT 11
 Q930K0 PRELIMINARY; PRT; 195 AA.
 AC Q930K0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative transposase.
 GN RA0195 OR SMA0360.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 NCBI_TaxID=382;
 RX SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RC MEDLINE=21396509; PubMed=11481432;
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
 RA Batloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
 RA Gurjal M., Hong A., Hutzar L., Hyman R.W., Kahn D., Kahn M.L.,
 RA Kaiman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
 RA Yeh K.-C., Davis R.W., Federapfel N.A., Long S.R.;
 RT "Nucleotide sequence and predicted functions of the entire
 Sinorhizobium meliloti pSyma megaplasmid,"
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
 DR EMBL; AB007212; AAK64853.1; -
 DR InterPro; IPR001584; Rve.
 DR Pfam; PF00665; rve; 1.
 KW Plasmid; Hypothetical protein; Complete proteome.
 SO SEQUENCE 195 AA; 22083 MW; 4F8481D656BEC9FD CRC64;

Query Match 70.6%; Score 36; DB 16; Length 195;

Best Local Similarity 77.8%; Pred. No. 27;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 GHRPLDKR 9
 |||||
 Db 46 GHRPLDKR 54

RESULT 12
 Q92XY9 PRELIMINARY; PRT; 201 AA.
 AC Q92XY9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative transcriptional regulator.
 GN RA1099 OR SMA2008.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 NCBI_TaxID=382;
 RX SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RC MEDLINE=21396509; PubMed=11481432;
 RA Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
 RA Batloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
 RA Gurjal M., Hong A., Hutzar L., Hyman R.W., Kahn D., Kahn M.L.,
 RA Kaiman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
 RA Yeh K.-C., Davis R.W., Federapfel N.A., Long S.R.;
 RT "Nucleotide sequence and predicted functions of the entire
 Sinorhizobium meliloti pSyma megaplasmid,"
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
 DR EMBL; AB007296; AAK65757.1; -
 DR InterPro; IPR001647; HTH_Tetr.
 DR Pfam; PF00440; tetr; 1.
 KW Plasmid; Hypothetical protein; Complete proteome.
 SO SEQUENCE 201 AA; 21500 MW; 447E9E9BF63BF551 CRC64;

Query Match 70.6%; Score 36; DB 16; Length 201;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GHRPLD 6
 |||||
 Db 175 GHRPLD 180

RESULT 13
 Q8SBA0 PRELIMINARY; PRT; 471 AA.
 AC Q8SBA0;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical 50.2 kDa protein.
 GN OSUNBA0042H09.17.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzoae; Oryza.
 NCBI_TaxID=4530;
 RX SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPONBARE;
 RA Beil C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
 RA Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
 RA Tsitrin T., Riggs F., Hsiao J., Zisemann V., Blunt S., Pai G.,
 RA Vanaken S.E., Utterback T.R., Feldblum T.V., Kalb E., Quackenbush J.,
 RA Salzberg S.L., White O., Frazer C.M.;
 RT "Oryza sativa chromosome 10 BAC OSUNBA0042H09 genomic sequence,"
 Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC079874; AAT79787.1; -
 KW Hypothetical protein
 SQ SEQUENCE 471 AA; 50200 MW; 75D92E78D51937DD CRC64;

Query Match
 Best Local Similarity 70.6%; Score 36; DB 10; Length 471;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
 |||||
 Db 32 GHRPLD 37

RESULT 14

Q9HA50 PRELIMINARY; PRT; 505 AA.
 AC Q9HA50;
 DT 01-MAR-2001 (TRENBLREL. 16, Created)
 DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
 DE CDNA FLJ12240 f1s, clone MAMMA1001271.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MAMMARY GLAND;
 RA Isegai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
 RA Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Matanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuno Y.,
 RA "NEDO human cDNA sequencing project."
 RT Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AK022302; BAB14006.1; -
 DR SEQUENCE 505 AA; 54782 MW; 43BAD948C0DFEB7 CRC64;
 SO

Query Match
 Best Local Similarity 70.6%; Score 36; DB 4; Length 505;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 8
 |||||
 Db 41 GHRPLSKQ 48

RESULT 15

Q8VJW0 PRELIMINARY; PRT; 694 AA.
 AC Q8VJW0;
 DT 01-MAR-2002 (TRENBLREL. 20, Created)
 DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)
 DE PPE family protein.
 DE PPE family protein.
 GN MT1857.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CDC 1551 / OSHKOSH;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Becher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 laboratory strains";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE007044; AAK46130.1; -
 DR TIGR; MT1857; -
 DR InterPro; IPR000568; ATPsynth_Asub.
 DR InterPro; IPR000030; Microbac_PPE.
 DR Pfam; PF00823; PPE; 1.
 DR PROSITE; PS00449; ATPASE_A; UNKNOWN 1.
 SQ SEQUENCE 694 AA; 73206 MW; 2FDAD94290A07359 CRC64;

Query Match
 Best Local Similarity 70.6%; Score 36; DB 16; Length 694;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDKR 9
 |||||
 Db 85 GHRPLDKR 93

Search completed: June 27, 2003, 17:18:05
 Job time : 23.6 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2003, 09:58:09 ; Search time 70 Seconds
(without alignments)
17.132 Million cell updates/sec

Title: US-10-019-439-2
Perfect score: 51
Sequence: 1 GHRPLDKKR 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
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21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	9	22	AA1980.DAT.*
2	51	100.0	10	16	AA1981.DAT.*
3	51	100.0	12	13	AA1982.DAT.*
4	51	100.0	12	14	AA1983.DAT.*
5	51	100.0	16	14	AA1984.DAT.*
6	51	100.0	28	14	AA1985.DAT.*
7	51	100.0	29	14	AA1986.DAT.*
8	51	100.0	30	14	AA1987.DAT.*
9	51	100.0	30	14	AA1988.DAT.*
10	51	100.0	118	21	AA1989.DAT.*

11	51	100.0	140	22	AA1990.DAT.*	Novel human secret
12	51	100.0	141	22	AA1991.DAT.*	Human polypeptide
13	51	100.0	150	21	AA1992.DAT.*	Human secreted pro
14	51	100.0	453	22	AA1993.DAT.*	Human protein SEQ
15	51	100.0	491	16	AA1994.DAT.*	Human fibrinogen B
16	51	100.0	451	22	AA1995.DAT.*	Human protein SEQ
17	51	100.0	495	22	AA1996.DAT.*	Human protein SEQ
18	51	100.0	495	22	AA1997.DAT.*	Human protein SEQ
19	51	100.0	495	22	AA1998.DAT.*	Human protein SEQ
20	51	100.0	539	22	AA1999.DAT.*	Human protein SEQ
21	41	80.4	7	8	AA2000.DAT.*	Sequence of fibrin
22	41	80.4	7	11	AA2001.DAT.*	Peptide antigenic
23	41	80.4	7	15	AA2002.DAT.*	Beta-peptide used
24	41	80.4	8	9	AA2003.DAT.*	Fibrin-specific ep
25	41	80.4	8	14	AA2004.DAT.*	Human fibrin beta
26	41	80.4	8	15	AA2005.DAT.*	Human fibrin beta
27	41	80.4	8	15	AA2006.DAT.*	Synthetic beta-pep
28	41	80.4	8	15	AA2007.DAT.*	Fibrin-specific ep
29	41	80.4	12	14	AA2008.DAT.*	Human fibrin beta
30	39	76.5	39	23	AA2009.DAT.*	Mouse homologue of
31	39	76.5	54	22	AA2010.DAT.*	Propionibacterium
32	37	72.5	474	22	AA2011.DAT.*	Drosophila melanog
33	37	72.5	474	22	AA2012.DAT.*	Drosophila melanog
34	37	72.5	923	22	AA2013.DAT.*	Drosophila melanog
35	36	70.6	11	21	AA2014.DAT.*	Fibrinogen-beta pe
36	36	70.6	11	21	AA2015.DAT.*	Fibronectin beta c
37	36	70.6	33	21	AA2016.DAT.*	Sequence block SBW
38	36	70.6	159	23	AA2017.DAT.*	Streptococcus poly
39	36	70.6	155	23	AA2018.DAT.*	Streptococcus poly
40	36	70.6	306	21	AA2019.DAT.*	S. avermitilis HPP
41	36	70.6	434	22	AA2020.DAT.*	Novel human diagno
42	36	70.6	505	22	AA2021.DAT.*	Human protein sequ
43	36	70.6	613	22	AA2022.DAT.*	Novel human diagno
44	36	70.6	1102	21	AA2023.DAT.*	Human ORFX ORF3050
45	36	70.6	1251	22	AA2024.DAT.*	Novel protein kina

ALIGNMENTS

RESULT 1	AA1980.DAT.*
AB198079	AB198079 standard; peptide; 9 AA.
ID	AB198079
XX	AB198079
AC	AB198079
XX	AB198079
DT	22-JUL-2002 (first entry)
XX	22-JUL-2002 (first entry)
DE	Residues 45-54 of human fibrinogen beta chain precursor.
XX	Anti-arthritis; anti-inflammatory; fibrin; rheumatoid polyarthritis;
KW	human, fibrinogen beta chain.
XX	human, fibrinogen beta chain.
OS	Homo sapiens.
XX	Homo sapiens.
PN	FR2795735-A1.
XX	FR2795735-A1.
PD	05-JAN-2001.
XX	05-JAN-2001.
PF	01-JUL-1999; 99FR-0008470.
XX	01-JUL-1999; 99FR-0008470.
PR	01-JUL-1999; 99FR-0008470.
XX	01-JUL-1999; 99FR-0008470.
PA	(UYTO-) UNIV TOULOUSE SABATIER PAUL.
XX	(UYTO-) UNIV TOULOUSE SABATIER PAUL.
PI	Serre G, Sebbaq M;
XX	Serre G, Sebbaq M;
DR	WPI; 2001-114394/13.
XX	WPI; 2001-114394/13.
PT	New citrulline-containing polypeptide from fibrin, useful for diagnosis
XX	and treatment of rheumatoid polyarthritis
XX	Example 1; Page 12; 23pp; French.

XX The present invention relates to a citrulline (Cit) containing
 CC polypeptide derived from all or part of the alpha- or beta-chains of
 CC fibrin by substitution of at least one arginine residue by Cit. The Cit
 CC containing polypeptides can be used for in vitro diagnosis of rheumatoid
 CC polyarthritis (RP), by detecting disease-specific autoantibodies, and
 CC therapeutically for neutralising the RP-associated autoimmune response.
 CC The present sequence is a fragment (residues 45-54) of the human
 CC fibrinogen beta chain precursor, which was used in an example from the
 CC invention.

XX Sequence 9 AA;

Query Match 100.0%; Score 51; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKR 9
 |||||
 Db 1 GHRPLDKR 9

RESULT 2
 AAW11931

XX ID AAW11931 standard; peptide; 10 AA.

XX AC AAW11931;

XX DT 02-APR-1997 (first entry)

XX DE Fibrinogen A-alpha-chain residues 17-26.

XX KW Monoclonal; antibody; human; soluble; fibrin; fibrinogen;
 KW urea-treated; des-AAB; A-alpha-chain; immunoassay; diagnosis;

XX KM disseminated intravascular coagulation.

XX OS Homo sapiens.

XX PN WO9512617-A1.

XX PD 11-MAY-1995.

XX PF 01-NOV-1994; 94WO-JP01844.

XX PR 02-NOV-1993; 93JP-0297325.

XX PA (IATR) IATRON LAB INC.

XX PI Imuzuka K, Ito Y, Kohno I, Soe G;

XX DR WPI; 1995-206667/27.

XX PT Monoclonal antibody reactive with soluble human fibrin - but not
 PT with fibrinogen, is useful for fibrin immunoassay in plasma
 PT specimens

XX PS Example 3; Page 15; 32pp; Japanese.

XX A novel monoclonal antibody (MAB) reacts with human soluble fibrin,
 CC but not with human fibrinogen. Specifically when the MAB reacts
 CC with urea-treated des-AAB fibrin the reaction is not inhibited by
 CC peptides corresponding to fibrinogen A-alpha-chain residues 17-26
 CC (AAW11931), B-beta-chain residues 15-24 (AAW11932) or gamma-chain
 CC residues 312-324 (AAW11933). The MAB is useful in immunoassays for
 CC soluble fibrin in plasma samples (e.g. by sandwich immunoassay),
 CC particularly for the diagnosis of pathological conditions such as
 CC disseminated intravascular coagulation.

XX Sequence 10 AA;

Query Match 100.0%; Score 51; DB 16; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00058;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKR 9
 |||||
 Db 1 GHRPLDKR 9

RESULT 3

XX ID AAR28629 standard; peptide; 12 AA.

XX AC AAR28629;

XX DT 22-MAR-1993 (first entry)

XX DE N-terminal human fibrin peptide.

XX KW bispecific hybrid monoclonal antibody; thrombolytic agent;
 KW cardiac infarction; arterial embolism; cerebral infarction;
 KW peripheral arterial/venous obstruction; retinal arterial obstruction.

XX OS Homo sapiens.

XX PN EP513778-A.

XX PD 19-NOV-1992.

XX PF 14-MAY-1992; 92EP-0108134.

XX PR 17-MAY-1991; 91JP-0112874.

XX PR 13-MAR-1992; 92JP-0055025.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX PI Iwasa S, Kurokawa T, Watanabe A;

XX DR WPI; 1992-383677/47.

XX PT Bi-specific antibody useful for treating thrombotic obstructive
 PT diseases e.g. cardiac infarction - comprises antithrombus
 PT antibody variable region and anti-thrombolytic substance antibody
 PT variable region with no heavy chain constant region domains 2 and
 PT 3

XX PS Disclosure; Page 3; 30pp; English.

XX CC This sequence represents an N-terminal peptide of human fibrin. It
 CC was used in the production of bispecific monoclonal antibodies which
 CC are specific for fibrins, but do not bind fibrinogen, and are
 CC specific for anti-thrombolytic substance. The compsn. contg. these
 CC Abs lacks the side effects of prior art Ab targetted thrombolytic
 CC agents and has enhanced thrombolytic activity.

XX CC agents and has enhanced thrombolytic activity.

XX CC agents and has enhanced thrombolytic activity.

XX CC agents and has enhanced thrombolytic activity.

XX CC agents and has enhanced thrombolytic activity.

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XX CC agents and has enhanced thrombolytic activity.

XX CC agents and has enhanced thrombolytic activity.

XX CC agents and has enhanced thrombolytic activity.

XX CC agents and has enhanced thrombolytic activity.

XX CC agents and has enhanced thrombolytic activity.

KM Tissue plasminogen activator; t-PA; mutein; fibrin; antigen;
 KM anti-fibrin; monoclonal antibody; hybridoma; thrombolysis
 KM antithrombotic agent; bispecific antibody.
 XX Synthetic.
 OS
 FH Key
 FH Region
 FT 1..11
 FT /note= "human fibrin beta-chain residues 1-11"
 FT Modified-site
 FT 12
 FT /note= "BSA carrier is attached to Cys"
 FT
 PN JPO5304992-A.
 XX
 PD 19-NOV-1993.
 XX
 PF 17-JUN-1992; 92JP-0158301.
 XX
 PR 20-JUN-1991; 91JP-0148936.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 DR WPI; 1993-408334/51.
 XX
 PT Hybrid monoclonal antibody - used for prepn. of thrombolytic drug
 PT having increased thrombolytic activity and specificity and
 PT reduced reactivity to fibrinogen
 XX
 PS Disclosure; Page 9; 38pp; Japanese.
 XX
 CC Human fibrin beta-chain N-terminal peptide (1-11)-Cys was
 CC synthesised and coupled to BSA for injection into mice. The peptide
 CC was used to raise antibodies to human fibrin. Monoclonal antibodies
 CC specific for fibrin are used in the production of bispecific
 CC monoclonal antibodies which also recognise truncated tPA muteins
 CC lacking the finger, EGF and Kringle 1 domains.
 CC
 SQ Sequence 12 AA;
 XX
 Query Match 100.0%; Score 51; DB 14; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00071;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDKKR 9
 Db 1 GHRPLDKKR 9
 XX
 RESULT 5
 AAR44830
 ID AAR44830 standard; peptide; 16 AA.
 XX
 AC AAR44830;
 XX
 DT 20-JUN-1994 (first entry)
 XX
 DE Human fibrin beta-chain internal peptide fragment.
 XX
 KM Tissue plasminogen activator; t-PA; mutein; fibrin; antigen;
 KM anti-fibrin; monoclonal antibody; hybridoma; thrombolysis
 KM antithrombotic agent; bispecific antibody.
 XX
 OS Synthetic.
 OS
 PN JPO5304992-A.
 XX
 PD 19-NOV-1993.
 XX
 PF 17-JUN-1992; 92JP-0158301.
 XX
 PR 20-JUN-1991; 91JP-0148936.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.

XX
 DR WPI; 1993-408334/51.
 XX
 PT Hybrid monoclonal antibody - used for prepn. of thrombolytic drug
 PT having increased thrombolytic activity and specificity and
 PT reduced reactivity to fibrinogen
 XX
 PS Disclosure; Page 9; 38pp; Japanese.
 XX
 CC Human fibrin internal peptide fragment was identified as a
 CC candidate immunogen to raise antibodies to human fibrin. Monoclonal
 CC antibodies specific for fibrin are used in the production of bispecific
 CC monoclonal antibodies which also recognise truncated tPA muteins
 CC lacking the finger, EGF and Kringle 1 domains.
 CC
 SQ Sequence 16 AA;
 XX
 Query Match 100.0%; Score 51; DB 14; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.00098;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDKKR 9
 Db 6 GHRPLDKKR 14
 XX
 RESULT 6
 AAR40010
 ID AAR40010 standard; peptide; 28 AA.
 XX
 AC AAR40010;
 XX
 DT 23-MAY-1994 (first entry)
 XX
 DE Scintigraph imaging agent specific binding peptide.
 XX
 KM Reagent; site imaging; technetium-99m labelled; peptide.
 KM
 XX Synthetic.
 OS
 FH Key
 FH Location/Qualifiers
 FT Modified-site 28
 FT /note= "C-terminal amide"
 FT
 PN WO9321962-A.
 XX
 PD 11-NOV-1993.
 XX
 PF 19-APR-1993; 93WO-US03687.
 XX
 PR 30-APR-1992; 92US-0871282.
 XX
 PA (DIAT-) DIATECH INC.
 XX
 PI Buttram S, Civitello ER, Dean RT, Lister-James J, McBride W;
 XX
 DR WPI; 1993-368429/46.
 XX
 KM Reagents for preparing scintigraphic imaging agents - contg.
 KM technetium-99m labelled peptide(s) contg. 3-100 aminoacid(s)
 KM
 PS Claim 35; Page 39; 55pp; English.
 XX
 CC The sequence is that of a specific binding peptide used as part of
 CC a reagent for preparing a scintigraphic imaging agent for imaging
 CC sites within a mammalian body. In this the peptide is covalently
 CC linked to a radiolabel-binding moiety which is capable of forming
 CC a complex with a radioisotope, pref. technetium-99m.
 CC
 SQ Sequence 28 AA;
 XX
 Query Match 100.0%; Score 51; DB 14; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.0018;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHRPLDKR 9
 Db 1 GHRPLDKR 9

RESULT 7
 AAR42547
 ID AAR42547 standard; Peptide; 29 AA.
 XX AAR42547;
 AC AAR42547;

DT 05-AUG-1994 (first entry)
 XX Leukocyte-binding peptide which can bind to technetium-99m.
 DE Leukocyte binding peptide; fibrinopeptide B chain; scintigraphic imaging;
 KW inflammation site; technetium 99m.
 XX OS Synthetic.

FT Key Location/Qualifiers
 FT Modified-site 1
 FT /label= OTHER
 FT /note= "BAT, i.e. N6,N9-bis(2-methyl-
 FT 2-mercaptoethyl)-6,9-diazanonanoic acid"
 FT Modified-site 29
 FT /note= "Arg-NH2"

FN WO9317719-A.
 XX 16-SEP-1993.
 PD 12-MAR-1993; 93WO-US02320.
 XX 13-MAR-1992; 92US-0851074.
 PR (DIAT-) DIATECH INC.

PI Buttram S, Dean RT, Lees RS, Lister-James J;
 DR WPL; 1993-303154/38.

PT Scintigraphic imaging agent for sites of inflammation -
 PT comprising leukocyte-binding peptide bound technetium-99m via
 PT binding moiety
 XX Claim 15; Page 31; 40pp; English.

CC New peptides are claimed which are leukocyte binding peptides
 CC having covalently bound to them a moiety which can bind a Tc-99m
 CC radiolabel. The peptides having Tc-99m bound to them are useful as
 CC scintigraphic imaging agents for imaging sites of infection and
 CC inflammation in the mammalian body, e.g. caused by ischaemia,
 CC inflammatory bowel disorder, arthritis or tumours.
 CC The present sequence is a specifically claimed example of
 CC such a peptide derived from fibrinopeptide B chain.

SO Sequence 29 AA;
 Query Match 100.0%; Score 51; DB 14; Length 29;
 Best Local Similarity 100.0%; Pred. No. 0.0019;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHRPLDKR 9
 Db 2 GHRPLDKR 10

RESULT 8
 AAR42546
 ID AAR42546 standard; Peptide; 30 AA.

XX AAR42546;
 AC AAR42546;
 XX 05-AUG-1994 (first entry)
 DT 05-AUG-1994 (first entry)
 XX Leukocyte-binding peptide which can bind to technetium-99m.
 DE Leukocyte binding peptide; fibrinopeptide B chain; scintigraphic imaging;
 KW inflammation site; technetium 99m.
 XX OS Synthetic.

FT Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "picolinoyl-Gly"
 FT Modified-site 2
 FT /note= "acetamidomethyl-Cys"

FN WO9317719-A.
 XX 16-SEP-1993.
 PD 12-MAR-1993; 93WO-US02320.
 XX 13-MAR-1992; 92US-0851074.
 PR (DIAT-) DIATECH INC.

PI Buttram S, Dean RT, Lees RS, Lister-James J;
 DR WPL; 1993-303154/38.

PT Scintigraphic imaging agent for sites of inflammation -
 PT comprising leukocyte-binding peptide bound technetium-99m via
 PT binding moiety

XX Claim 15; Page 31; 40pp; English.
 CC New peptides are claimed which are leukocyte binding peptides
 CC having covalently bound to them a moiety which can bind a Tc-99m
 CC radiolabel. The peptides having Tc-99m bound to them are useful as
 CC scintigraphic imaging agents for imaging sites of infection and
 CC inflammation in the mammalian body, e.g. caused by ischaemia,
 CC inflammatory bowel disorder, arthritis or tumours.
 CC The present sequence is a specifically claimed example of
 CC such a peptide derived from fibrinopeptide B chain.

SO Sequence 30 AA;
 Query Match 100.0%; Score 51; DB 14; Length 30;
 Best Local Similarity 100.0%; Pred. No. 0.002;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHRPLDKR 9
 Db 3 GHRPLDKR 11

RESULT 9
 ABB11339
 ID ABB11339 standard; peptide; 87 AA.

XX ABB11339;
 AC ABB11339;
 DT 11-JAN-2002 (first entry)
 XX Human beta-fibrinogen homologue, SEQ ID NO:1709.

DE Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;

KM chronic inflammatory condition; proliferative retinopathy;
 KM atherosclerosis; coronary heart disease; arterial ischaemia;
 KM bone disorder; osteoporosis; vascular growth disorder;
 KM tissue regeneration; wound healing; infection; immune disorder;
 KM cell culture; drug screening; gene therapy; antiinflammatory;
 KM anaesthetic; antithrombotic; haemostatic; antiatherosclerotic;
 KM cytosolic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
 KM antifungal; vulnary; antiflcer.
 OS Homo sapiens.
 XX WO200157188-A2.
 PN 09-AUG-2001.
 PD 05-FEB-2001; 2001WO-US03800.
 PF 03-FEB-2000; 2000US-046914.
 PR 27-APR-2000; 2000US-0560875.
 XX (HYSE-) HYSEQ INC.
 PA Tang YT, Liu C, Drmanac RT;
 PI WPI; 2001-457740/49.
 DR N-PSDB; ABA08583.
 XX Human proteins and DNA encoding sequences useful for preventing,
 PT treating or ameliorating a medical condition in a mammalian subject
 PT e.g. arthritis and cancer -
 XX Claim 20; Page 167; 1963pp; English.
 PS Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA0825-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoietic regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention.
 XX Sequence 87 AA;

Query Match 100.0%; Score 51; DB 22; Length 87;
 Best Local Similarity 100.0%; Pred. No. 0.0063;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GHRPLDKR 9
 Db 31 GHRPLDKR 39
 RESULT 10
 ID AAG00151 standard; Protein; 118 AA.
 AC AAG00151;
 DT 06-OCT-2000 (first entry)
 DE Human secreted protein, SEQ ID NO: 4232.
 XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KM gene therapy; chromosome mapping.
 OS Homo sapiens.
 XX EP1033401-A2.
 PN 06-SEP-2000.
 PD 21-FEB-2000; 2000EP-0200610.
 PF 26-FEB-1999; 99US-0122487.
 PR (GEST) GENSET.
 PA Dumas Milne Edwards J, Duclert A, Giordano J;
 PI WPI; 2000-500381/45.
 DR N-PSDB; AAC00157.
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX Claim 13; SEQ ID 4232; 71pp + CD-ROM; English.
 CC The present sequence is a polypeptide encoded by one of a large number
 CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
 CC were prepared from total human RNAs or polyA+ RNAs derived from 30
 CC different tissues. EST sequences usually correspond mainly to the 3'
 CC untranslated region (UTR) of the mRNA because they are often obtained
 CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
 CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
 CC those cases where longer cDNA sequences have been obtained, the full 5'
 CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
 CC ends and can therefore be used to obtain full length cDNAs and genomic
 CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
 CC chromosome mapping procedures. They are used to obtain upstream
 CC regulatory sequences and to design expression and secretion vectors.
 XX Sequence 118 AA;
 Qy 1 GHRPLDKR 9
 Db 45 GHRPLDKR 53
 RESULT 11
 ID AAU33273 standard; Protein; 140 AA.
 Query Match 100.0%; Score 51; DB 21; Length 118;
 Best Local Similarity 100.0%; Pred. No. 0.0088;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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XX AC AA03273;
XX DT 18-DEC-2001 (first entry)
XX DE Novel human secreted protein #3764.
XX KW Human; vaccination; gene therapy; nutritional supplement;
XX KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX OS Homo sapiens.
XX PN WO200179449-A2.
XX PD 25-OCT-2001.
XX PF 16-APR-2001; 2001WO-US08656.
XX PR 18-APR-2000; 2000US-0552928.
XX PR 26-JAN-2001; 2001US-0770160.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT;
XX DR WPI; 2001-611725/70.
XX PT Nucleic acids encoding a range of human polypeptides, useful in genetic
XX PS vaccination, testing and therapy.
XX SS Claim 20; Page 752; 765pp; English.
CC The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation; to regulate haematopoiesis; and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration; and in
CC immune suppression and/or stimulation; as anti-inflammatory agents; and in
CC in treatment of leukaemias. AA029510-AA03304 represent the amino acid
CC sequences of novel human secreted proteins of the invention.
XX SQ Sequence 140 AA;
XX
XX Query Match
XX Best Local Similarity 100.0%; Score 51; DB 22; Length 140;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GHRPLDKKR 9
XX DB 45 GHRPLDKKR 53
XX
XX RESULT 12
XX ID AA010778 standard; Protein; 141 AA.
XX AC AA010778;
XX DT 06-NOV-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 24670.
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;

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XX KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX KW tissue growth factor; immunomodulatory; cancer; leukaemia;
XX KW nervous system disorders; arthritis; inflammation.
XX OS Homo sapiens.
XX PN WO200164835-A2.
XX PD 07-SEP-2001.
XX PF 26-FEB-2001; 2001WO-US04927.
XX PR 28-FEB-2000; 2000US-0515126.
XX PR 18-MAY-2000; 2000US-0577409.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Drmanac RT;
XX DR WPI; 2001-514838/56.
XX DR N-PSDB; AA190709.
XX PT Isolated nucleic acids and polypeptides, useful for preventing
XX PT diagnosing and treating e.g. leukaemia, inflammation and immune
XX PS disorders.
XX SS Claim 20; SEQ ID NO 24670; 1399pp + Sequence Listing; English.
CC The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AA000010-AA033910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoietic regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhibit activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pat_sequences.
XX SQ Sequence 141 AA;
XX
XX Query Match
XX Best Local Similarity 100.0%; Score 51; DB 22; Length 141;
XX Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GHRPLDKKR 9
XX DB 41 GHRPLDKKR 49
XX
XX RESULT 13
XX ID AAG00150 standard; Protein; 150 AA.
XX AC AAG00150;
XX DT 06-OCT-2000 (first entry)
XX DE Human secreted protein, SEQ ID NO: 4231.
XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX KW gene therapy; chromosome mapping.
XX OS Homo sapiens.
XX PN EP1033401-A2.
XX PR 06-SEP-2000.
XX PD
XX

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PF 21-FEB-2000; 2000EP-0200610.
 XX
 XX 26-FEB-1999; 99US-0122487.
 PR
 XX (GEST) GENSET.
 PA
 XX
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX
 DR WPI; 2000-500381/45.
 DR N-PSDB; AAC00156.
 XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX
 XX
 PS Claim 13; SEQ ID 4231; 71bp + CD-ROM; English.
 XX
 CC The present sequence is a polypeptide encoded by one of a large number
 CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
 CC were prepared from total human RNAs or polyA+ RNAs derived from 30
 CC different tissues. EST sequences usually correspond mainly to the 3'
 CC untranslated region (UTR) of the mRNA because they are often obtained
 CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
 CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
 CC those cases where longer cDNA sequences have been obtained, the full 5'
 CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
 CC ends and can therefore be used to obtain full length cDNAs with genomic
 CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
 CC chromosome mapping procedures. They are used to obtain upstream
 CC regulatory sequences and to design expression and secretion vectors.
 XX
 SQ Sequence 150 AA;
 Query Match 100.0%; Score 51; DB 21; Length 150;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDKKR 9
 |||||
 Db 45 GHRPLDKKR 53

RESULT 14
 AAM78493
 ID AAM78493 standard; Protein; 453 AA.
 XX
 AC AAM78493;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human protein SEQ ID NO 1155.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN MO200157190-A2.
 PD
 XX
 PD 09-AUG-2001.
 PD
 XX
 PF 05-FEB-2001; 2001MO-US04098.
 PF
 XX
 PR 03-FEB-2000; 2000US-0496914.
 PR
 PR 27-APR-2000; 2000US-0560875.
 PR
 PR 20-JUN-2000; 2000US-0598075.
 PR
 PR 19-JUL-2000; 2000US-0620335.
 PR
 PR 01-SEP-2000; 2000US-0654936.
 PR
 PR 15-SEP-2000; 2000US-0663561.
 PR
 PR 20-OCT-2000; 2000US-0693325.
 PR
 PR 30-NOV-2000; 2000US-0728422.
 PR

XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PI Zhao QA, Wang D, Wang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Weinman T, Goodrich R;
 XX
 DR WPI; 2001-476283/51.
 DR
 DR N-PSDB; AAK51626.
 XX
 PT Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX
 XX
 PS Claim 20; Page 3390-3391; 6221bp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAK00302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.
 XX
 SQ Sequence 453 AA;
 Query Match 100.0%; Score 51; DB 22; Length 453;
 Best Local Similarity 100.0%; Pred. No. 0.039;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDKKR 9
 |||||
 Db 45 GHRPLDKKR 53

RESULT 15
 AAR82243
 ID AAR82243 standard; Protein; 491 AA.
 XX
 AC AAR82243;
 XX
 DT 26-OCT-1996 (first entry)
 XX
 DE Human fibrinogen B-beta chain protein.
 XX
 KW Human fibrinogen B-beta chain; transgenic animal milk; treatment;
 KW sheep beta-lactoglobulin signal peptide fusion protein;
 KW surgical adhesive.
 XX
 OS Homo sapiens.
 XX
 PN MO9523868-A1.
 PD
 XX
 PD 08-SEP-1995.
 PD
 XX
 PF 01-MAR-1995; 95MO-US02648.
 PF
 XX
 PR 03-MAR-1994; 94US-0206176.
 PR
 XX
 PA (PHAR-) PHARM PROTEINS LTD.
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Dalrymple MA, Foster DC, Garner I, Prunkard DE;
 DR WPI; 1995-320582/41.
 DR
 DR N-PSDB; AAT03852.
 XX

PT Production of fibrinogen in transgenic mammals - by introducing DNA
PT segments into the germ line of a non-human mammal and collecting
PT milk from female progeny.

XX Disclosure; Page 55-57; 99pp; English.

CC Human fibrinogen B-beta chain may be produced recombinantly,
CC preferably by sheep beta-lactoglobulin signal peptide fusion
CC protein gene expression in non-human transgenic animal milk,
CC preferably of a sheep, pig, goat or cattle. Co-expression with the
CC fibrinogen A-alpha chain (see AAR82244) and the gamma chain (see
CC AAR82245) results in the production of active fibrinogen, which is
CC useful in human and veterinary medicine, e.g. in the formulation of
CC surgical adhesives, which also consist of Factor XIII, and as a
CC coating surface for polymeric articles, such as synthetic vascular
CC grafts.

SQ Sequence 491 AA;

Query Match

Best Local Similarity 100.0%; Score 51; DB 16; Length 491;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKR 9
DB 45 GHRPLDKR 53

RESULT 16

AAM78492

ID AAM78492 standard; Protein; 491 AA.

AC AAM78492;

DT 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 1154.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorder; arthritis; inflammation.

OS Homo sapiens.
XX
XX WO200157190-A2.

PD 09-AUG-2001.

PF 05-FEB-2001; 2001WO-US04098.

PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.

XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Dimanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y,
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhtman T, Goodrich R;
DR WPI, 2001-476283/51.
DR N-PSDB; AAK51625.

PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX Claim 2; Page 3389-3390; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.

CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.

SQ Sequence 491 AA;

Query Match

Best Local Similarity 100.0%; Score 51; DB 22; Length 491;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKR 9
DB 45 GHRPLDKR 53

RESULT 17

AAM79475

ID AAM79475 standard; Protein; 495 AA.

AC AAM79475;

DT 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 3121.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorder; arthritis; inflammation.

OS Homo sapiens.

XX WO200157190-A2.

PD 09-AUG-2001.

PF 05-FEB-2001; 2001WO-US04098.

PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.

XX (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Dimanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y,
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhtman T, Goodrich R;
DR WPI, 2001-476283/51.
DR N-PSDB; AAK52608.

PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX Claim 20; Page 257-258; 6221pp; English.

CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
XX
SQ Sequence 495 AA;

Query Match 100.0%; Score 51; DB 22; Length 495;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKR 9
Db 49 GHRPLDKR 57
|||||
|

RESULT 18
AAM79476
ID AAM79476 standard; Protein: 495 AA.
XX
XX AAM79476;
XX
XX
DT 06-NOV-2001 (first entry)
XX
XX Human protein SEQ ID NO 3122.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX KM tissue growth factor; immunomodulatory; cancer; leukaemia;
XX KW nervous system disorder; arthritis; inflammation.
XX
XX Homo sapiens.
XX OS
XX
XX WO200157190-A2.
XX
XX
XX PD 09-AUG-2001.
XX
XX
XX PF 05-FEB-2001; 2001WO-US04098.
XX
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XX PR 03-FEB-2000; 2000US-0496914.
XX PR 27-APR-2000; 2000US-0560875.
XX PR 20-JUN-2000; 2000US-0598075.
XX PR 19-JUL-2000; 2000US-0620325.
XX PR 01-SEP-2000; 2000US-0654936.
XX PR 15-SEP-2000; 2000US-0663561.
XX PR 20-OCT-2000; 2000US-0693325.
XX PR 30-NOV-2000; 2000US-0728422.
XX
XX
XX PA (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
XX PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX PI Xue AJ, Yang Y, Wejhtman T, Goodrich R;
XX
XX WPI; 2001-476283/51.
XX DR N-PSDB; AAK52609.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
XX PT useful in diagnosis and gene therapy -
XX
XX Claim 20; Page 258; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the

CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
XX
SQ Sequence 495 AA;

Query Match 100.0%; Score 51; DB 22; Length 495;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKR 9
Db 49 GHRPLDKR 57
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RESULT 19
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ID AAM79477 standard; Protein: 495 AA.
XX
XX AAM79477;
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XX
DT 06-NOV-2001 (first entry)
XX
XX Human protein SEQ ID NO 3123.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX KM tissue growth factor; immunomodulatory; cancer; leukaemia;
XX KW nervous system disorder; arthritis; inflammation.
XX
XX Homo sapiens.
XX OS
XX
XX WO200157190-A2.
XX
XX
XX PD 09-AUG-2001.
XX
XX
XX PF 05-FEB-2001; 2001WO-US04098.
XX
XX
XX PR 03-FEB-2000; 2000US-0496914.
XX PR 27-APR-2000; 2000US-0560875.
XX PR 20-JUN-2000; 2000US-0598075.
XX PR 19-JUL-2000; 2000US-0620325.
XX PR 01-SEP-2000; 2000US-0654936.
XX PR 15-SEP-2000; 2000US-0663561.
XX PR 20-OCT-2000; 2000US-0693325.
XX PR 30-NOV-2000; 2000US-0728422.
XX
XX
XX PA (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
XX PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX PI Xue AJ, Yang Y, Wejhtman T, Goodrich R;
XX
XX WPI; 2001-476283/51.
XX DR N-PSDB; AAK52610.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
XX PT useful in diagnosis and gene therapy -
XX
XX Claim 20; Page 258; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to

CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
CC
SQ Sequence 495 AA;
Query Match 100.0%; Score 51; DB 22; Length 495;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GHRPLDKR 9
DB 49 GHRPLDKR 57
RESULT 20
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ID AAM78491 standard; Protein: 539 AA.
XX
AC AAM78491;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1153.
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KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN W0200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Dimaac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y,
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI: 2001-476283/51.
DR N-PSDB; AAK51624.
XX
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
XX Claim 20; Page 3388-3389; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce

CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
CC
SQ Sequence 539 AA;
Query Match 100.0%; Score 51; DB 22; Length 539;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GHRPLDKR 9
DB 93 GHRPLDKR 101

Search completed: June 29, 2003, 09:59:29
Job time : 72 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 17:18:12 ; Search time 27.9 Seconds
(without alignments)
35.370 Million cell updates/sec

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Perfect score: 51
Sequence: 1 GHRPLDKR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 424699 seqs, 109646833 residues

Total number of hits satisfying chosen parameters: 424699

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	51	100.0	20	US-10-142-935-6	Sequence 6, Appli
2	51	100.0	25	US-10-142-935-4	Sequence 4, Appli
3	51	100.0	30	US-10-131-543-5	Sequence 5, Appli
4	51	100.0	30	US-10-131-546-5	Sequence 5, Appli
5	51	100.0	30	US-10-131-546-5	Sequence 5, Appli
6	51	100.0	30	US-10-131-546-5	Sequence 5, Appli
7	51	100.0	488	US-09-919-039-33	Sequence 33, Appli
8	51	100.0	491	US-10-017-724-6	Sequence 6, Appli
9	36	70.6	10	US-10-142-935-9	Sequence 9, Appli
10	36	70.6	15	US-10-142-935-8	Sequence 8, Appli
11	36	70.6	20	US-10-142-935-5	Sequence 5, Appli
12	36	70.6	66	US-10-213-512-296	Sequence 296, App
13	36	70.6	66	US-09-071-838-296	Sequence 296, App
14	34	66.7	54	US-09-864-761-34308	Sequence 34308, A
15	34	66.7	256	US-09-350-874-32	Sequence 32, Appli
16	34	66.7	3354	US-10-160-758-11	Sequence 11, Appli
17	34	66.7	3354	US-10-160-758-12	Sequence 12, Appli
18	33	64.7	68	US-10-102-806-465	Sequence 465, App
19	33	64.7	385	US-10-147-003-2	Sequence 2, Appli

20	32	62.7	239	9	US-10-233-131-28	Sequence 28, Appli
21	32	62.7	318	9	US-09-738-626-4955	Sequence 4955, Ap
22	32	62.7	855	10	US-10-072-094-9	Sequence 9, Appli
23	32	62.7	855	10	US-09-817-913-13	Sequence 13, Appli
24	32	62.7	855	10	US-09-817-538-13	Sequence 13, Appli
25	32	62.7	967	9	US-09-563-728A-30	Sequence 30, Appli
26	32	62.7	967	10	US-09-817-913-7	Sequence 7, Appli
27	32	62.7	967	10	US-09-817-538-7	Sequence 7, Appli
28	32	62.7	1084	9	US-10-072-094-7	Sequence 7, Appli
29	32	62.7	1084	9	US-10-173-539-12	Sequence 12, Appli
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36	32	62.7	1352	10	US-09-736-968A-9	Sequence 9, Appli
37	32	62.7	1354	9	US-09-736-968A-10	Sequence 10, Appli
38	32	62.7	1534	10	US-09-736-968A-10	Sequence 10, Appli
39	32	62.7	1534	10	US-09-736-968A-10	Sequence 10, Appli
40	32	62.7	1980	9	US-09-736-968A-108	Sequence 108, Appli
41	32	62.7	1980	10	US-09-736-968A-94	Sequence 94, Appli
42	32	62.7	1980	10	US-09-736-968A-91	Sequence 91, Appli
43	32	62.7	2008	9	US-09-736-968A-105	Sequence 105, Appli
44	32	62.7	2008	9	US-09-978-244A-29	Sequence 29, Appli
45	32	62.7	2008	10	US-09-736-968A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-142-935-6
; Sequence 6, Application US/10142935
; Publication No. US2003004418A1
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULAT
; FILE REFERENCE: P072010US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-6

Query Match 100.0%; Score 51; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKR 9
DB 10 GHRPLDKR 18

RESULT 2
US-10-142-935-4
; Sequence 4, Application US/10142935
; Publication No. US2003004418A1
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULAT
; FILE REFERENCE: P072010US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072

; PRIOR FILING DATE: 2001-05-13
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 25
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus epidermidis
 US-10-142-935-4

Query Match
 Best Local Similarity 100.0%; Score 51; DB 9; Length 25;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKR 9
 Db 15 GHRPLDKR 23

RESULT 3
 US-10-131-543-5
 ; Sequence 5, Application US/10131543
 ; Publication No. US20030072709A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cyr, John E.
 ; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
 ; FILE REFERENCE: 09744-016001
 ; CURRENT APPLICATION NUMBER: US/10/131,543
 ; PRIOR FILING DATE: 2002-04-24
 ; PRIOR APPLICATION NUMBER: US 09/694,992
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: PCT/US01/50423
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 30
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic construct
 ; NAME/KEY: AMIDATION
 ; LOCATION: 30
 US-10-131-543-5

Query Match
 Best Local Similarity 100.0%; Score 51; DB 9; Length 30;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKR 9
 Db 4 GHRPLDKR 12

RESULT 4
 US-10-131-346-5
 ; Sequence 5, Application US/10131346
 ; Publication No. US20030103899A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cyr, John E.
 ; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
 ; FILE REFERENCE: 09744-017001
 ; CURRENT APPLICATION NUMBER: US/10/131,346
 ; PRIOR FILING DATE: 2002-04-24
 ; PRIOR APPLICATION NUMBER: US 09/695,360
 ; PRIOR FILING DATE: 2000-10-24
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 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: FastSeq for Windows Version 4.0

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 ; LENGTH: 30
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic construct
 ; NAME/KEY: AMIDATION
 ; LOCATION: 30
 US-10-131-346-5

Query Match
 Best Local Similarity 100.0%; Score 51; DB 9; Length 30;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKR 9
 Db 4 GHRPLDKR 12

RESULT 5
 US-10-131-546-5
 ; Sequence 5, Application US/10131546
 ; Publication No. US20030103895A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cyr, John E.
 ; TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
 ; FILE REFERENCE: 09744-018001
 ; CURRENT APPLICATION NUMBER: US/10/131,546
 ; PRIOR FILING DATE: 2002-04-24
 ; PRIOR APPLICATION NUMBER: US 09/695,494
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: PCT/US01/50423
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 30
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic construct
 ; NAME/KEY: AMIDATION
 ; LOCATION: 30
 US-10-131-546-5

Query Match
 Best Local Similarity 100.0%; Score 51; DB 9; Length 30;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKR 9
 Db 4 GHRPLDKR 12

RESULT 6
 US-09-919-039-33
 ; Sequence 33, Application US/09919039
 ; Publication No. US20030108871A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaser, Matthew R.
 ; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
 ; FILE REFERENCE: PA-0035 US
 ; CURRENT APPLICATION NUMBER: US/09/919,039
 ; PRIOR FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: 60/222,113
 ; NUMBER OF SEQ ID NOS: 401
 ; SOFTWARE: PERL Program

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; SEQ ID NO 33
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 3393861CD1
US-09-919-039-33

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```

Query Match          100.0%; Score 51; DB 9; Length 488;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GHRPLDKKR 9
        |||||
Db      42 GHRPLDKKR 50

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RESULT 7
US-10-017-724-6
; Sequence 6, Application US/10017724
; Publication No. US2003009958A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Jeanette
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE
; FILE REFERENCE: MMI-004
; CURRENT APPLICATION NUMBER: US/10/017,724
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/317,178
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/329,958
; PRIOR FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-017-724-6

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Query Match          100.0%; Score 51; DB 9; Length 491;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GHRPLDKKR 9
        |||||
Db      45 GHRPLDKKR 53

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RESULT 8
US-10-142-935-9
; Sequence 9, Application US/10142935
; Publication No. US20030044418A1
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-9

```

```

Query Match          70.6%; Score 36; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GHRPLD 6
        |||||
Db      5 GHRPLD 10

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RESULT 9
US-10-142-935-8
; Sequence 8, Application US/10142935
; Publication No. US20030044418A1
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-8

```

```

Query Match          70.6%; Score 36; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      1 GHRPLD 6
        |||||
Db      10 GHRPLD 15

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```

RESULT 10
US-10-142-935-5
; Sequence 5, Application US/10142935
; Publication No. US20030044418A1
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Stacey
; APPLICANT: HOOK, Magnus A.O.
; TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULATION
; FILE REFERENCE: P07201US01/BAS
; CURRENT APPLICATION NUMBER: US/10/142,935
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,072
; PRIOR FILING DATE: 2001-05-13
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-142-935-5

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Query Match          70.6%; Score 36; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 GHRPLD 6
        |||||
Db      15 GHRPLD 20

```

```

RESULT 11
US-10-213-512-296
; Sequence 296, Application US/10213512
; Publication No. US20030110536A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Ohad, Nir

```

APPLICANT: Kiyosue, Tomohiro
 APPLICANT: Yadegari, Ramlin
 APPLICANT: Margossian, Linda
 APPLICANT: Harada, John
 APPLICANT: Goldberg, Robert B.
 TITLE OF INVENTION: The Regents of the University of California
 TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
 FILE REFERENCE: 023070-086100US
 CURRENT APPLICATION NUMBER: US/10/213,512
 CURRENT FILING DATE: 2002-08-06
 PRIOR APPLICATION NUMBER: US/09/177,206
 PRIOR FILING DATE: 1998-10-22
 PRIOR APPLICATION NUMBER: US 09/071,838
 PRIOR FILING DATE: 1998-05-01
 NUMBER OF SEQ ID NOS: 324
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 296
 LENGTH: 66
 TYPE: PRT
 ORGANISM: Arabidopsis sp.
 US-10-213-512-296

Query Match 70.6%; Score 36; DB 9; Length 66;
 Best Local Similarity 85.7%; Pred. No. 5.5;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPDLKX 8
 DB 48 HRPLEKK 54

RESULT 12

US-09-071-838-296
 Sequence 296; Application US/09071838
 Patent No. US20020152501A1
 GENERAL INFORMATION:
 APPLICANT: Fischer, Robert L.
 APPLICANT: Ohad, Nir
 APPLICANT: Kiyosue, Tomohiro
 APPLICANT: Yadegari, Ramlin
 APPLICANT: Margossian, Linda
 APPLICANT: Harada, John
 APPLICANT: Goldberg, Robert B.
 TITLE OF INVENTION: Nucleic Acids That Control Seed and
 TITLE OF INVENTION: Fruit Development in Plants
 NUMBER OF SEQUENCES: 324
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/071,838
 FILING DATE: 01-MAY-1998
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Bastian, Kevin L.
 REGISTRATION NUMBER: 34,774
 REFERENCE/DOCKET NUMBER: 023070-086100US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 296:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 66 amino acids

TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-071-838-296

Query Match 70.6%; Score 36; DB 10; Length 66;
 Best Local Similarity 85.7%; Pred. No. 5.5;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPDLKX 8
 DB 48 HRPLEKK 54

RESULT 13

US-09-799-875-5
 Sequence 5; Application US/09799875
 Patent No. US20020034780A1
 GENERAL INFORMATION:
 APPLICANT: Meyers, Rachel
 APPLICANT: Kapeller-Libermann, Rosana
 APPLICANT: Williamson, Mark
 TITLE OF INVENTION: No. US20020034780A1 Human Protein Kinases and Uses
 TITLE OF INVENTION: Therefor
 FILE REFERENCE: 35800/209996
 CURRENT APPLICATION NUMBER: US/09/799,875
 CURRENT FILING DATE: 2001-03-06
 PRIOR APPLICATION NUMBER: 60/182,059
 PRIOR FILING DATE: 2000-02-11
 PRIOR APPLICATION NUMBER: 09/659,287
 PRIOR FILING DATE: 2000-09-12
 NUMBER OF SEQ ID NOS: 32
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 5
 LENGTH: 1203
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-799-875-5

Query Match 70.6%; Score 36; DB 10; Length 1203;
 Best Local Similarity 75.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDKX 8
 DB 799 GHRPLSKQ 806

RESULT 14

US-09-864-761-34308
 Sequence 34308; Application US/09864761
 Patent No. US20020048763A1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharon G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 FILE REFERENCE: Aeomica-X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263.6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34308
; LENGTH: 54
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009238.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 6.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN HEILA, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 62
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
; OTHER INFORMATION: EST_HUMAN HIT: A1002818.1, EVALU6 5.00e-24
US-09-864-761-34308

Query Match      66.7%; Score 34; DB 10; Length 54;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 GHRPLDKK 8
Db      15 GHTPLSKK 22

RESULT 15
US-09-350-874-32
; Sequence 32, Application US/09350874
; Patent No. US20020019020A1
; GENERAL INFORMATION:
; APPLICANT: Rhodes, Kenneth
; APPLICANT: An, Mengdian
; TITLE OF INVENTION: METHODS FOR TREATING CARDIOVASCULAR DISORDERS
; FILE REFERENCE: NMI-069
; CURRENT APPLICATION NUMBER: US/09/350,874
; EARLIER FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: USSN 60/110,277
; EARLIER FILING DATE: 1998-11-30
; EARLIER APPLICATION NUMBER: USSN 60/110,033
; EARLIER FILING DATE: 1998-11-25
; EARLIER APPLICATION NUMBER: USSN 60/109,333
; EARLIER FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: USSN 09/298,731
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; EARLIER FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-350-874-32

Query Match      66.7%; Score 34; DB 10; Length 256;
Best Local Similarity 75.0%; Pred. No. 61;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy      1 GHRPLDKK 8
Db      20 GHTPLSKK 27

Search completed: June 27, 2003, 17:30:22
Job time : 28.9 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 17:15:46 ; Search time 9.9 Seconds
(without alignments)
26.748 Million cell updates/sec

Title: US-10-019-439-2

Perfect score: 51

Sequence: 1 GHRLPKKR 9

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued Patents AA.*
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3: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	10	2	US-08-448-547-1
2	51	100.0	28	1	US-08-486-135-12
3	51	100.0	28	1	US-08-470-152-12
4	51	100.0	28	2	US-08-468-9648-10
5	51	100.0	28	2	US-07-871-282A-10
6	51	100.0	28	2	US-08-290-853-33
7	51	100.0	28	2	US-08-253-678A-10
8	51	100.0	28	3	US-08-582-134B-10
9	51	100.0	28	3	US-08-170-299-10
10	51	100.0	30	2	US-08-290-853-35
11	51	100.0	31	1	US-08-472-535-9
12	51	100.0	31	1	US-08-484-774-9
13	51	100.0	31	3	US-08-266-178A-9
14	51	100.0	491	1	US-08-206-176-4
15	41	80.4	7	1	US-08-058-699-10
16	41	80.4	8	1	US-08-058-699-11
17	36	70.6	66	4	US-09-177-249-96
18	34	66.7	200	4	US-09-298-731-32
19	34	66.7	236	4	US-09-399-913-32
20	33	64.7	155	4	US-09-315-794-12
21	33	64.7	155	4	US-09-389-341-12
22	32	62.7	215	1	US-08-107-684B-9
23	32	62.7	215	1	US-08-107-684B-13
24	31	60.8	170	1	US-08-227-372-1
25	31	60.8	170	6	5194425-3
26	31	60.8	219	4	US-09-134-001C-4644
27	31	60.8	265	4	US-09-199-637A-369

28	30	58.8	21	1	US-08-507-124-4	Sequence 4, Appli
29	30	58.8	28	4	US-09-227-357-357	Sequence 357, App
30	30	58.8	117	4	US-09-199-637A-33	Sequence 33, Appl
31	30	58.8	253	4	US-09-180-109A-35	Sequence 35, Appl
32	30	58.8	254	4	US-09-180-109A-31	Sequence 31, Appl
33	30	58.8	288	1	US-08-368-852-15	Sequence 15, Appl
34	30	58.8	288	2	US-08-525-940-15	Sequence 15, Appl
35	30	58.8	300	4	US-08-976-838-15	Sequence 15, Appl
36	30	58.8	358	2	US-09-227-357-348	Sequence 348, App
37	30	58.8	358	4	US-08-558-823-19	Sequence 19, Appl
38	30	58.8	393	3	US-08-979-817A-4	Sequence 4, Appli
39	30	58.8	460	1	US-08-476-008-50	Sequence 50, Appl
40	30	58.8	460	1	US-08-306-063-50	Sequence 50, Appl
41	30	58.8	460	1	US-08-833-485-50	Sequence 50, Appl
42	30	58.8	460	4	US-09-137-440-50	Sequence 50, Appl
43	30	58.8	463	4	US-09-163-444-2	Sequence 2, Appli
44	30	58.8	545	2	US-08-990-114-1	Sequence 1, Appli
45	30	58.8	545	4	US-09-241-333-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-448-547-1
Sequence 1, Application US/08448547
Patent No. 5623068
GENERAL INFORMATION:
APPLICANT: Soe, Gilbu
APPLICANT: Kohno, Isao
APPLICANT: Inuzuka, Kimiko
APPLICANT: Ito, Yumiko
TITLE OF INVENTION: ~~ANGIOTENSIN SOLUBLE FIBRIN ANTIBODY~~
TITLE OF INVENTION: HYBRIDOMA, AND IMMUNOASSAYING METHOD
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,547
FILING DATE: 30-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/01844
FILING DATE: 01-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-297325
FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: Q-38931
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-448-547-1

Query Match 100.0%; Score 51; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDKR 9
Db 1 GHRPLDKR 9

RESULT 2

US-08-486-135-12
; Sequence 12, Application US/08486135
; Patent No. 5720934
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,135
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5720934nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,205-N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-486-135-12

Query Match 100.0%; Score 51; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDKR 9
Db 1 GHRPLDKR 9

RESULT 3

US-08-470-152-12
; Sequence 12, Application US/08470152
; Patent No. 5780007
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R

; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Allegretti, Ltd.
; STREET: 10 South Wacker Drive, Suite 3000
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,152
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5780007nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 92,205-L
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELEX: 910-221-5317
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-470-152-12

Query Match 100.0%; Score 51; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDKR 9
Db 1 GHRPLDKR 9

RESULT 4

US-08-468-964B-10
; Sequence 10, Application US/08468964B
; Patent No. 5922303
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: Buttram, Scott
; APPLICANT: McBride, William
; APPLICANT: Lister-James, John
; APPLICANT: Civitello, Edgar R.
; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Diatide, Inc.
; STREET: 9 Delta Drive
; CITY: Londonderry
; STATE: NH
; COUNTRY: USA
; ZIP: 03053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,964B
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: DITI 111D4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (603) 437-8970
TELEFAX: (603) 437-8977
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-468-964B-10

Query Match 100.0%; Score 51; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKR 9
DB 1 GHRPLDKR 9

RESULT 5
US-07-871-282A-10
Sequence 10, Application US/07871282A
Patent No. 5965107
GENERAL INFORMATION:
APPLICANT: Dean, Richard T.
APPLICANT: Buttram, Scott
APPLICANT: McBride, William
APPLICANT: Lister-James, John
APPLICANT: Civitello, Edgar R.
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
TITLE OF INVENTION: Imaging
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Diatide, Inc.
STREET: 9 Delta Drive
CITY: Londonderry
STATE: NH
COUNTRY: USA
ZIP: 03053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/871,282A
FILING DATE: 20-APR-1992
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: McDaniel, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: DITI 111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (603) 437-8970
TELEFAX: (603) 437-8977
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-871-282A-10

Query Match 100.0%; Score 51; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKR 9
DB 1 GHRPLDKR 9

RESULT 6
US-08-290-853-33
Sequence 33, Application US/08290853
Patent No. 5989519
GENERAL INFORMATION:
APPLICANT: Dean, Richard T.
APPLICANT: Buttram, Scott
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
TITLE OF INVENTION: Imaging Inflammation
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,853
FILING DATE: 11-OCT-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: No. 5989519nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,112-H
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= BAT
OTHER INFORMATION: /note= "The amino terminus is linked to a BAT
OTHER INFORMATION: radiolabel binding moiety."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 28
OTHER INFORMATION: /label= Amide
OTHER INFORMATION: /note= "The carboxyl terminus is modified to an
OTHER INFORMATION: amide"
US-08-290-853-33

Query Match 100.0%; Score 51; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKR 9
DB 1 GHRPLDKR 9

RESULT 7
US-08-253-678A-10
Sequence 10, Application US/08253678A
Patent No. 5997844

GENERAL INFORMATION:
APPLICANT: Dean, Richard T.
APPLICANT: Buttram, Scott
APPLICANT: McBride, William
APPLICANT: Lister-James, John
APPLICANT: Civilello, Edgar R.
TITLE OF INVENTION: TECHNETIUM-99m LABELED PEPTIDES FOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dialide, Inc.
STREET: 9 Delta Drive
CITY: Londonderry
STATE: NH
COUNTRY: USA
ZIP: 03053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,678A
FILING DATE: 03-JUN-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Mcdaniels, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: DITI 112
TELECOMMUNICATION INFORMATION:
TELEPHONE: (603) 437-8970
TELEFAX: (603) 437-8977
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-253-678A-10

Query Match 100.0%; Score 51; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKKR 9
Db 1 GHRPLDKKR 9

RESULT 8
US-08-582-134B-10
Sequence 10, Application US/08582134B
Patent No. 6074627
GENERAL INFORMATION:
APPLICANT: Dean, Richard T.
APPLICANT: Buttram, Scott
APPLICANT: McBride, William
APPLICANT: Lister-James, John
APPLICANT: Civilello, Edgar R.
TITLE OF INVENTION: TECHNETIUM-99m LABELED PEPTIDES FOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dialide, Inc.
STREET: 9 Delta Drive
CITY: Londonderry
STATE: NH
COUNTRY: USA
ZIP: 03053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/582,134B
FILING DATE: 14-MAY-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Mcdaniels, Patricia A.
REGISTRATION NUMBER: 33,194
REFERENCE/DOCKET NUMBER: DITI 112D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (603) 437-8970
TELEFAX: (603) 437-8977
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-582-134B-10

Query Match 100.0%; Score 51; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKKR 9
Db 1 GHRPLDKKR 9

RESULT 9
US-08-170-299-10
Sequence 10, Application US/08170299
Patent No. 6086849
GENERAL INFORMATION:
APPLICANT: Dean, Richard T.
APPLICANT: Buttram, Scott
APPLICANT: McBride, William
APPLICANT: Lister-James, John
APPLICANT: Civilello, Edgar R.
TITLE OF INVENTION: Technetium-99m labeled Peptides for
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegrecti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/170,299
FILING DATE: 09-FEB-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 6086849nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,205-H
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-170-299-10

Query Match 100.0%; Score 51; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.0018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKKR 9
|||||
DB 1 GHRPLDKKR 9

RESULT 10
US-08-290-853-35

Sequence 35, Application US/08290853
Patent No. 5989519

GENERAL INFORMATION:

APPLICANT: Dean, Richard T

APPLICANT: Buttram, Scott

TITLE OF INVENTION: Technetium-99m Labeled Peptides for

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti, Ltd.

STREET: 10 South Wacker Drive, Suite 3000

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/290.853

FILING DATE: 11-OCT-1994

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: No. 5989519nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 92,112-H

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1..3

OTHER INFORMATION: /label= Picolinoyl

OTHER INFORMATION: /note= "The amino terminal residue is

OTHER INFORMATION: pyridine-2-carbonyl; the thiol of the cysteine is

OTHER INFORMATION: protected by an acetamidomethyl group."

FEATURE:

NAME/KEY: Modified-site

LOCATION: 30

OTHER INFORMATION: /label= Amide

OTHER INFORMATION: /note= "The carboxyl terminus is modified to an

OTHER INFORMATION: amide"

US-08-290-853-35

Query Match 100.0%; Score 51; DB 2; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.0019;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKKR 9
|||||

DB 3 GHRPLDKKR 11

RESULT 11

US-08-472-535-9

Sequence 9, Application US/08472535

Patent No. 5711931

GENERAL INFORMATION:

APPLICANT: Dean, Richard T

APPLICANT: Lees, Robert S.

APPLICANT: Buttram, Scott

TITLE OF INVENTION: Technetium-99m Labeled Peptides for

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti, Ltd.

STREET: 10 South Wacker Drive, Suite 3000

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472.535

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: No. 5711931nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 92,112-J

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 31 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1..3

OTHER INFORMATION: /label= Picolinoyl

OTHER INFORMATION: /note= "The amino terminal residue is

OTHER INFORMATION: pyridine-2-carbonyl; the thiol of the cysteine

OTHER INFORMATION: residue is protected by an acetamidomethyl

US-08-472-535-9

Query Match 100.0%; Score 51; DB 1; Length 31;

Best Local Similarity 100.0%; Pred. No. 0.002;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKKR 9
|||||

DB 4 GHRPLDKKR 12

RESULT 12

US-08-484-774-9

Sequence 9, Application US/08484774

Patent No. 5807538

GENERAL INFORMATION:

APPLICANT: Dean, Richard T

APPLICANT: Buttram, Scott

TITLE OF INVENTION: Technetium-99m Labeled Peptides for

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,774
FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: No. 5807538nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,112-K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:

NAME/KEY: Modified-site
LOCATION: 1..3

OTHER INFORMATION: /label= Pico11noy1

OTHER INFORMATION: /note= "The amino terminal residue is
pyridine-2-carbonyl; the thiol of the cysteine
residue is protected by an acetamidomethyl

US-08-484-774-9

Query Match

Best Local Similarity 100.0%; Score 51; DB 1; Length 31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GHRPLDKKR 9
|||||||
Db 4 GHRPLDKKR 12

RESULT 13

US-08-266-178A-9
Sequence 9, Application US/08266178A
Patent No. 6017510

GENERAL INFORMATION:

APPLICANT: Dean, Richard T
TITLE OF INVENTION: Buttram, Scott
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
NUMBER OF INVENTION: Imaging Inflammation
CORRESPONDENCE ADDRESS: 17
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/266,178A
FILING DATE: 27-JUN-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: No. 6017510nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,112
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
TELEX: 910-221-5317

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:

NAME/KEY: Modified-site
LOCATION: 1..3

OTHER INFORMATION: /label= Pico11noy1

OTHER INFORMATION: /note= "The amino terminal residue is
pyridine-2-carbonyl; the thiol of the cysteine
residue is protected by an acetamidomethyl

US-08-266-178A-9

Query Match

Best Local Similarity 100.0%; Score 51; DB 3; Length 31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GHRPLDKKR 9
|||||||
Db 4 GHRPLDKKR 12

RESULT 14

US-08-206-176-4
Sequence 4, Application US/08206176
Patent No. 5639940

GENERAL INFORMATION:

APPLICANT: Garner, Ian
TITLE OF INVENTION: Dalrymple, Michael A
APPLICANT: Prunkard, Donna E
TITLE OF INVENTION: Foster, Donald C
TITLE OF INVENTION: Production of Fibrinogen in Transgenic
NUMBER OF INVENTION: Animals
CORRESPONDENCE ADDRESS: 27
ADDRESSEE: ZymoGenetics, Inc.
STREET: 4225 Roosevelt Way, N.E.
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,176
FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Parker, Gary E
REGISTRATION NUMBER: 31-648
REFERENCE/DOCKET NUMBER: 93-15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-547-8080 ext 322
TELEFAX: 206-548-2329

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 491 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-206-176-4

Query Match 100.0%; Score 51; DB 1; Length 491;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKR 9
|||||
Db 45 GHRPLDKR 53

RESULT 15
US-08-058-699-10
; Sequence 10, Application US/08058699
; Patent No. 5443827
; GENERAL INFORMATION:
; APPLICANT: Edgar Haber
; APPLICANT: Christoph Bode
; APPLICANT: Marschall S. Runge
; TITLE OF INVENTION: FIBRIN-TARGETED INHIBITORS OF
; TITLE OF INVENTION: THROMBIN
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/058,699
; FILING DATE: 19930503
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: N/A
; FILING DATE: N/A
; ATTORNEY/AGENT INFORMATION:
; NAME: Janis K. Fraser, Ph.D.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 05433/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: Linear
US-08-058-699-10

Query Match 80.4%; Score 41; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
|||||
Db 1 GHRPLDK 7

Search completed: June 27, 2003, 17:19:04
Job time : 10.9 secs

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OM protein - protein search, using sw model

Run on: June 27, 2003, 17:29:22 ; Search time 38 Seconds
(without alignments)
27.828 Million cell updates/sec.

Title: US-10-019-439-1

Perfect score: 57

Sequence: 1 GPRVERHOSA 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 1326

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	35.1	10	2 JN0440	peptide-N4-(N-acet
2	19	33.3	10	1 XASNPC	angiotensin-conver
3	19	33.3	11	2 PC4267	ribosomal protein
4	19	33.3	11	2 I54193	Rhesus blood group
5	18	31.6	10	2 B56899	serum heterodimer,
6	18	31.6	11	2 PU0029	33K protein 3218 -
7	18	31.6	11	2 PT0302	Ig heavy chain CRD
8	17	29.8	11	2 A14454	6-phosphofructokin
9	16	28.1	6	2 A37765	hypothetical prote
10	16	28.1	8	2 S66646	cardioacceleratory
11	16	28.1	8	2 B45800	serum albumin - do
12	16	28.1	9	2 A60427	macrophage cytocto
13	16	28.1	11	2 S21127	precortin methyltr
14	16	28.1	11	2 E41476	probable antigen 5
15	16	28.1	11	2 PS0259	39K protein 3225 -
16	15	26.3	7	2 A44428	platelet aggregati
17	15	26.3	8	2 A28719	thymic humoral fac
18	15	26.3	8	2 I57532	gene Tnfrs10a
19	15	26.3	9	2 PT0315	Ig heavy chain prote
20	15	26.3	10	2 S63478	diacylglycerol
21	15	26.3	10	2 PH1592	Ig H chain V-D-J r
22	14	24.6	5	2 C41225	copper resistance
23	14	24.6	7	2 A34818	vicillin 72K chain
24	14	24.6	7	2 PQ0727	H2 class I protein
25	14	24.6	7	2 A33098	244K exantigen -
26	14	24.6	7	2 B33541	hypothetical prote
27	14	24.6	7	2 B48394	major lat-globule
28	14	24.6	7	2 C35389	urease (EC 3.5.1.5
29	14	24.6	10	2 S48182	bacterioferritin -

30	14	24.6	10	2 PT0284	Ig heavy chain CRD
31	14	24.6	10	2 C54823	olfactory receptor
32	14	24.6	10	2 D54823	olfactory receptor
33	14	24.6	11	1 XAV1BH	bradykinin-potent
34	14	24.6	11	2 YHRT	morphogenetic neur
35	14	24.6	11	2 YHRT	morphogenetic neur
36	14	24.6	11	2 YHBO	morphogenetic neur
37	14	24.6	11	2 YHXA	morphogenetic neur
38	14	24.6	11	2 YHUFHY	morphogenetic neur
39	14	24.6	11	2 J00395	hypothetical prote
40	14	24.6	11	2 H54346	pyruvate synthase
41	14	24.6	11	2 PC2173	triacylglycerol li
42	14	24.6	11	2 S09024	carboxylesterase (
43	13	22.8	4	2 PT0675	T-cell receptor be
44	13	22.8	5	2 PT0267	Ig heavy chain CRD
45	13	22.8	5	2 J05020	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

JN0440
peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) - sweet almond
N;Alternate names: glycopeptidase
C;Species: Prunus dulcis var. sativa (sweet almond)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 19-May-2000
C;Accession: JN0440
R;Kalliberda, E.I.; Shemyakin, V.V.; Antonov, V.K.
B;Georg. Khim. 16, 751-757, 1990
A;Title: Purification of sweet almond glycopeptidase and sequencing of N-terminal prote
A;Reference number: JN0440
A;Accession: JN0440
A;Molecule type: protein
A;Residues: 1-10 <KAL>
C;Keywords: hydrolase

Query Match

Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRV 5
Db 3 PRV 6

RESULT 2

XASNPC
angiotensin-converting enzyme inhibitor - aspic viper
C;Species: Viperas aspic (aspic viper)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 08-Dec-1995
C;Accession: A60377
R;Komori, Y.; Sugihara, H.
Int. J. Biochem. 22, 767-771, 1990
A;Title: Characterization of a new inhibitor for angiotensin converting enzyme from the
A;Reference number: A60377, PMID:90382616; PMID:2169439
A;Accession: A60377
A;Molecule type: protein
A;Residues: 1-10 <KOM>
C;Superfamily: bradykinin-potentiating peptide
C;Keywords: angiotensin-converting enzyme inhibitor; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match

Best Local Similarity 75.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRV 4
Db 5 GPRV 8

RESULT 3

PC4267
ribosomal protein L12.1 - rice (fragment)
C:Species: Oryza sativa (rice)
C:Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 18-Jul-1997
C:Accession: PC4267
R:Kawakami, T.; Kamo, M.; Chen, M.C.; Tsugita, A.
submitted to JIPID, April 1997
A:Reference number: PC4267
A:Accession: PC4267
A:Molecule type: protein
A:Residues: 1-11 <KAW>
A:Experimental source: strain Japonica Nihonbare

Query Match 33.3%; Score 19; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRVVE 6
|||
Db 7 PRVLE 11

RESULT 4
I54193
Rhesus blood group CcEe protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
C:Accession: I54193
R:Cherif-Zahar B.; Le Van Kim, C.; Rouillac, C.; Raynal, V.; Cartton, J.P.; Colin, Y.
Genomics 19, 68-74, 1994
A:Title: Organization of the gene (RHCE) encoding the human blood group RnCcEe antigens
A:Reference number: I54193; MUID:94245182; PMID:8188244
A:Accession: I54193
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-11 <RES>
A:Cross-references: GB:S70456; NID:9546795; PIDN:AMD14061.1; PID:94261761
C:Genetics:
A:Gene: GDB:RHCE
A:Cross-references: GDB:229957; OMIM:111700
A:Map position: 1p36.2-1p34

Query Match 33.3%; Score 19; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRVER 7
|||
Db 6 PRSVR 11

RESULT 5
B56899
serum heterodimer, 24k chain - sandbar shark (fragment)
C:Species: Carcharias plumbeus (sandbar shark)
C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 20-Jun-2000
C:Accession: B56899
R:Vazquez-Moreno, L.; Porath, J.; Schluter, S.F.; Marchalonis, J.J.
Comp. Biochem. Physiol. B 103, 563-568, 1992
A:Title: Purification of a novel heterodimer from shark (Carcharias plumbeus) serum by
A:Reference number: A56899; MUID:93092592; PMID:1458832
A:Accession: B56899
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <VAX>
C:Keywords: glycoprotein; plasma

Query Match 31.6%; Score 18; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.5e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPRV 5
|||

Db 4 GERVV 8

RESULT 6
P00029
33k protein 3218 - rice (strain Nihonbare) (fragment)
C:Species: Oryza sativa (rice)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C:Accession: P00029
R:Tsugita, A.; Miyatake, N.
submitted to JIPID, April 1993
A:Reference number: P00208
A:Accession: P00029
A:Molecule type: protein
A:Residues: 1-11 <TSU>
A:Experimental source: bran
C:Comment: molecular weight 33K, pI 6.0.

Query Match 31.6%; Score 18; DB 2; Length 11;
Best Local Similarity 42.9%; Pred. No. 3.2e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPRV 7
|||
Db 5 GPRXHQ 11

RESULT 7
PT0302
Ig heavy chain CDR3 region (clone 5-112) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0302
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0302
A:Molecule type: DNA
A:Residues: 1-11 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotrimer; immunoglobulin

Query Match 31.6%; Score 18; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPR 3
|||
Db 3 GPR 5

RESULT 8
A14454
6-phosphofructokinase (EC 2.7.1.11) - sheep (fragment)
C:Species: Ovis orientalis aries; Ovis ammon aries (domestic sheep)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 28-Apr-1993
C:Accession: A14454
R:Poodyce, A.M.; Midwinter, G.G.; Moore, C.H.
Biochem. Soc. Trans. 7, 721-723, 1979
A:Title: The N-terminal amino acid sequence of sheep heart phosphofructokinase.
A:Reference number: A14454; MUID:80004524; PMID:157899
A:Accession: A14454
A:Molecule type: protein
A:Residues: 1-11 <FOR>
C:Keywords: glycolysis; phosphotransferase

Query Match 29.8%; Score 17; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ERHQA 11
|||

Db 3 EHHHEA 8

RESULT 9

A37765
 hypothetical protein (cema 5' region) - Chloroflexus aurantiacus (fragment)
 C/Species: Chloroflexus aurantiacus
 C/Date: 31-May-1991 #sequence_revision 31-May-1991 #text_change 30-Sep-1993
 C/Accession: A37765
 R/theroux, S.J.; Redlinger, T.E.; Fuller, R.C.; Robinson, S.J.
 J. Bacteriol. 172, 4497-4504, 1990
 A/Title: Gene encoding the 5.7-kilodalton chlorosome protein of Chloroflexus aurantiacus
 A/Reference number: A37765; PMID:90350558; PMID:237656
 A/Accession: A37765
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-6 <THS>
 A/Cross-references: GB:M33964

Query Match 28.1%; Score 16; DB 2; Length 6;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 PRVER 7
 Db 1 PQMAOR 6

RESULT 10

S66646
 cardioacceleratory protein 2b - tobacco hornworm
 C/Species: Manduca sexta (tobacco hornworm)
 C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
 C/Accession: S66646
 R/Ruesmann, G.R.; Cheung, C.C.; Loi, P.K.; Lee, T.D.; Swiderick, K.M.; Tublitz, N.J.
 FEBS Lett. 371, 311-314, 1995
 A/Title: Amino acid sequence of CAP(2b), an insect cardioacceleratory peptide from the C
 A/Reference number: S66646; PMID:96013159; PMID:7556618
 A/Accession: S66646
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-8 <HDE>

Query Match 28.1%; Score 16; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRV 4
 Db 6 PRV 8

RESULT 11

B45800
 serum albumin - dog (fragment)
 C/Species: Canis lupus familiaris (dog)
 C/Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 31-Dec-1993
 C/Accession: B45800
 R/Carraway, R.E.; Cochran, D.E.; Boucher, W.; Mitra, S.P.
 J. Immunol. 143, 1680-1684, 1989
 A/Title: Structures of histamine-releasing peptides formed by the action of acid proteas
 A/Reference number: A45800; PMID:89341406; PMID:2474609
 A/Accession: B45800
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-8 <CAR>

Query Match 28.1%; Score 16; DB 2; Length 8;
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 VVERH 8
 Db 1

Db 1 IARRH 5

RESULT 12

A60427
 macrophage cytotoxicity-inducing factor, 29K - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Jun-1993
 C/Accession: A60427
 R/Jones, C.M.; Prince, C.A.; Williams, J.S.
 Exp. Hematol. 19, 704-709, 1991
 A/Title: Purification and amino acid analysis of a human macrophage cytotoxicity-induci
 A/Reference number: A60427; PMID:91372335; PMID:1909970
 A/Accession: A60427
 A/Molecule type: protein
 A/Residues: 1-9 <JON>
 A/Note: the sequence from the text on page 706 is inconsistent with that from page 708
 C/Keywords: cytokine

Query Match 28.1%; Score 16; DB 2; Length 9;
 Best Local Similarity 44.4%; Pred. No. 2.8e+05;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPRVERHQ 9
 Db 1 GAVALDSQ 9

RESULT 13

S21127
 precorrin methyltransferase - Salmonella typhimurium
 C/Species: Salmonella typhimurium
 C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
 C/Accession: S21127
 R/Roesener, C.A.; Warren, M.J.; Santander, P.J.; Atshaves, B.P.; Ozaki, S.; Stelowich,
 FEBS Lett. 301, 73-78, 1992
 A/Title: Expression of 9 Salmonella typhimurium enzymes for cobinamide synthesis. Ident
 A/Reference number: S21127; PMID:93083628; PMID:1451790
 A/Accession: S21127
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-11 <ROE>

Query Match 28.1%; Score 16; DB 2; Length 11;
 Best Local Similarity 40.0%; Pred. No. 7.7e+03;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PRVE 6
 Db 7 PORIE 11

RESULT 14

B41476
 probable antigen 5 - Mycobacterium leprae (fragment)
 C/Species: Mycobacterium leprae
 C/Date: 10-Apr-1992 #sequence_revision 10-Apr-1992 #text_change 18-Jun-1993
 C/Accession: B41476
 R/Hartbeek, R.A.; van Rens, R.M.; Stabel, L.F.E.M.; de Wit, M.Y.L.; Klatser, P.R.
 Infect. Immun. 58, 2821-2827, 1990
 A/Title: Selection and characterization of recombinant clones that produce Mycobacteriu
 A/Reference number: A41476; PMID:90354041; PMID:1696931
 A/Accession: B41476
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: DNA
 A/Residues: 1-11 <HAR>

Query Match 28.1%; Score 16; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 7.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRV 4
 Db 1

Db 5 PRV 7

RESULT 15

PS0259

39K protein 3225 - rice (strain Nihonbare) (fragment)

C/Species: Oryza sativa (rice)

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995

C/Accession: PS0259

R/Tsugita, A.; Kamo, M.

submitted to JIPID, April 1993

A/Reference number: PS0209

A/Accession: PS0259

A/Molecule type: protein

A/Residues: 1-11 <TSU>

A/Experimental source: callus

C/Comment: molecular weight 39K, pI 5.7.

Query Match

Best Local Similarity 28.1%; Score 16; DB 2; Length 11;

Matches 3; Conservativity 50.0%; Pred. No. 7.7e+03;

1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPRVE 6

Db 6 GPRVAD 11

Search completed: June 27, 2003, 17:34:17
Job time : 39 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 17:26:47 ; Search time 22 Seconds
(without alignments)
20.738 Million cell updates/sec

Title: US-10-019-439-1
Perfect score: 57
Sequence: 1 GPRVHERHQA 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 411

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	20	35.1	8 1 FAR7_ASCSU	P43171 Ascaris suu
2	19	33.3	8 1 UH09_RAT	P6575 Rattus norv
3	19	33.3	10 1 BPP_VIPAS	P13151 Vipera aspi
4	18	31.6	9 1 FAR9_ASCSU	P43172 Ascaris suu
5	16	28.1	9 1 NEUX_HUMAN	P04277 Homo sapien
6	15	26.3	10 1 URA6_HUMAN	P32080 Homo sapien
7	14	24.6	7 1 UF03_MOUSE	P38641 Mus musculu
8	14	24.6	10 1 UPAS_HUMAN	P30091 Homo sapien
9	14	24.6	10 1 URE3_MORMO	P17339 Morganelia
10	14	24.6	11 1 BPP_AGKHP	P04562 Agkistrodon
11	14	24.6	11 1 MOR1_HUMAN	P01163 Homo sapien
12	13	22.8	7 1 MNPL_LBPRD	P42984 Leptinotars
13	13	22.8	7 1 UH11_RAT	P6576 Rattus norv
14	13	22.8	8 1 AL15_CARMA	P61818 Carcinus ma
15	13	22.8	8 1 AL16_CARMA	P61819 Carcinus ma
16	13	22.8	8 1 AL15_CALVO	P41841 Calliphora
17	13	22.8	8 1 AL18_CARMA	P61811 Carcinus ma
18	13	22.8	8 1 AL19_CARMA	P61812 Carcinus ma
19	13	22.8	8 1 LMT2_LOCOMI	P22396 Locusta mig
20	13	22.8	8 1 LPK_LEUMA	P13049 Leucophaea
21	13	22.8	8 1 LPK2_PERAM	P32697 Periplaneta
22	13	22.8	8 1 LPK3_PERAM	P32698 Periplaneta
23	13	22.8	8 1 R57_MYCIT	P33564 Mycobacteri
24	13	22.8	8 1 VGL6_HSV2B	P61780 Herpes simp
25	13	22.8	9 1 LMT3_LOCOMI	P41489 Locusta mig
26	13	22.8	9 1 LPK1_PERAM	P26291 Periplaneta
27	13	22.8	9 1 TKL1_LOCOMI	P16223 Locusta mig
28	13	22.8	9 1 XYLA_STRSQ	P19149 Streptomyce
29	13	22.8	10 1 COXM_RAT	P60431 Rattus norv
30	13	22.8	10 1 COXO_RAT	P60432 Rattus norv
31	13	22.8	10 1 COXO_THIOB	P60982 Thynnus obe
32	13	22.8	10 1 LPK2_LOCOMI	P41488 Locusta mig
33	13	22.8	10 1 TRP8_LEUMA	P41740 Leucophaea

34	13	22.8	11 1	ANGT_CRIGE	F09037 crinia geor
35	13	22.8	11 1	BPP3_BOTIN	P30423 bothrops in
36	13	22.8	11 1	BPP4_BOTIN	P30424 bothrops in
37	13	22.8	11 1	PKC1_CARMO	P26684 carausius m
38	13	22.8	11 1	TKNA_ONCMY	P28429 oncorhynch
39	13	22.8	11 1	UN05_CLOPA	P81350 clostridium
40	12	21.1	4 1	TUFT_HUMAN	P01858 homo sapien
41	12	21.1	5 1	BIOB_CITFR	P01858 homo sapien
42	12	21.1	7 1	FAR2_ASCSU	P12997 citrobacter
43	12	21.1	7 1	LANC_CARUI	P1890 ascaris suu
44	12	21.1	7 1	UF04_MOUSE	P36660 carnobacter
45	12	21.1	8 1	GLUR_HUMAN	P38642 mus musculu
					P02729 homo sapien

ALIGNMENTS

```

RESULT 1
FAR7_ASCSU
ID FAR7_ASCSU STANDARD; PRT; 8 AA.
AC P43171;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRFamide-like neuropeptide AF7.
OS Ascaris suum (pig roundworm) (Ascaris lumbricoidea).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RX MEDLINE=95380362; Pubmed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Bright novel FMRFamide-like neuropeptides isolated from the nematode
RT Ascaris suum."
RL Peptides 16:491-500 (1995).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD RES 8
SQ SEQUENCE 8 AA; 963 MW; 9CD40059D417687D CRC64;

Query Match 35.1%; Score 20; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPRV 5
Db 2 GPRFI 6

RESULT 2
UH09_RAT
ID UH09_RAT STANDARD; PRT; 8 AA.
AC P6575;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot P9) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RX SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleisner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to the SWISS-PROT data bank
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 8.9; ITS MW IS: 42 KDa.
FT NON TER 8
SQ SEQUENCE 8 AA; 1029 MW; 9E0775A6C4140B06 CRC64;

```

Query Match 33.3%; Score 19; DB 1; Length 8;
 Best Local Similarity 80.0%; Pred. No. 1.1e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 ERHOS 10
 |||
 2 ERROS 6

Db

RESULT 3
 BPP VIPAS STANDARD; PRT; 10 AA.
 ID BPP VIPAS
 AC P31351;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Bradykinin-potentiating peptide (Angiotensin-converting
 enzyme inhibitor).
 OS Vipera aspis (Aspic viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Viperidae; Viperinae; Vipera.
 OX NCBI_TaxID=8706;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90382616; PubMed=2169439;
 RA Komori Y., Sugihara H.;
 RT "Characterization of a new inhibitor for angiotensin converting
 enzyme from the venom of Vipera aspis aspis.";
 RL Int. J. Biochem. 22:767-771(1990).
 CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
 ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
 BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
 CC IF ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
 DR PIR; A60377; XASNPC.
 KW Hypotensive agent; Venom.
 FT MOD_RES 1
 SQ SEQUENCE 10 AA; 1062 MW; 3BA827C327686773 CRC64;

Query Match 33.3%; Score 19; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 6.1e+02;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPRV 4
 |||
 5 GPKV 8

Db

RESULT 4
 FAR9 ASCSU STANDARD; PRT; 9 AA.
 ID FAR9 ASCSU
 AC P43172;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE FMRFamide-like neuropeptide Af9.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae;
 OC Ascaridae; Ascaris.
 OX NCBI_TaxID=6253;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95380362; PubMed=7651904;
 RA Cowden C., Stretton A.O.W.;
 RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
 Ascaris suum.";
 RL Peptides 16:491-500(1995).
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 9
 SQ SEQUENCE.

SO SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;

Query Match 31.6%; Score 18; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPR 3
 |||
 3 GPR 5

Db

RESULT 5
 NEUX HUMAN STANDARD; PRT; 9 AA.
 ID NEUX HUMAN
 AC P04277;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neurotensin-related peptide (NRP) (Kinetensin).
 OS Homo sapiens (Human).
 OS Bos taurus (Bovine), and
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606, 9913, 9986;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Human;
 RX MEDLINE=86242180; PubMed=3087352;
 RA Mogard M.H., Kobayashi R., Chen C.F., Lee T.D., Reeve J.R. Jr.,
 RA Shively J.E., Walsh J.H.;
 RT "The amino acid sequence of kinetensin, a novel peptide isolated from
 peptin-treated human plasma: homology with human serum albumin,
 neurotensin and angiotensin.";
 RL Biochem. Biophys. Res. Commun. 136:983-988(1986).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=Human, Bovine, and Rabbit;
 RX MEDLINE=87194805; PubMed=2437111;
 RA Carraway R.E., Miltz S.P., Cochran D.E.;
 RT "Structure of a biologically active neurotensin-related peptide
 obtained from pepsin-treated albumin(s).";
 RL J. Biol. Chem. 262:5968-5973(1987).
 CC -1- FUNCTION: REGULATION OF FAT DIGESTION, LIPID ABSORPTION, AND
 BLOOD FLOW (POTENTIAL).
 CC PIR; A03239; ABRUSK.
 DR PIR; A26693; A26693.
 KW Hormone.
 FT MOD_RES 9 AA; 1172 MW; C804DB4761F4140D CRC64;

Query Match 28.1%; Score 16; DB 1; Length 9;
 Best Local Similarity 40.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 VVERH 8
 |||
 1 IARRH 5

Db

RESULT 6
 URA6 HUMAN STANDARD; PRT; 10 AA.
 ID URA6 HUMAN
 AC P32080;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of red blood cells (Spot 17) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.

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RC TISSUE=Erythrocyte;
RA MEDLINE=94147970; PubMed=8313871;
RA Golaz O., Hughes G.J., Frutiger S., Paquet N., Bairoch A.,
RA Pasquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C.,
RA Balant L., Hochstrasser D.F.;
RT "Plasma and red blood cell protein maps: update 1993.";
CC Electrophoresis 14:1223-1231(1993).
RL -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.4, ITS MW IS: 65 kDa.
DR SWISS-2DPAGE; P32080; HUMAN.
FT NON_TER
SQ SEQUENCE 10 AA; 965 MW; 63DDC8D86AE1EDDB CRC64;

Query Match 26.6%; Score 15; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ERHSA 11
DB 3 EAHXGA 8

RESULT 7
UF03_MOUSE STANDARD; PRT; 7 AA.
AC P38641;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (936) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RA MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.1, ITS MW IS: 36 kDa.
FT NON_TER
SQ SEQUENCE 7 AA; 842 MW; 6AA72B1DDB1B180 CRC64;

Query Match 24.6%; Score 14; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 HOSA 11
DB 1 HEEA 4

RESULT 8
UPA5_HUMAN STANDARD; PRT; 10 AA.
AC P30091;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 13) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RA MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,

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RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochstrasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 4.85, ITS MW IS: 40 kDa.
CC -1- MISCELLANEOUS: THIS SPOT IS ON A POSITION THOUGHT TO BE THAT OF
CC 2N-ALPHA-2 GLYCOPROTEIN, BUT IT DOES NOT CORRESPOND TO THAT
CC PROTEIN.
DR SWISS-2DPAGE; P30091; HUMAN.
FT NON_TER
FT VARIANT 9 9 G->Y. /FTId=VAR_000002.
SQ SEQUENCE 10 AA; 1109 MW; C3DA94C73C32776 CRC64;

Query Match 24.6%; Score 14; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 5.8e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRVY 5
DB 4 PKVL 7

RESULT 9
URE3_MORMO STANDARD; PRT; 10 AA.
AC P17335;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Urease gamma subunit (EC 3.5.1.5) (6 kDa subunit) (Urea
DE amidohydrolase) (Fragment).
GN UREA.
OS Morganella morganii (Proteus morganii).
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Morganella.
OX NCBI_TaxId=582;
RN [1]
RP SEQUENCE.
RX MEDLINE=90264298; PubMed=2345135;
RA Hu L.-T., Nicholson E.B., Jones B.D., Lynch M.J., Mobley H.L.T.;
RT "Morganella morganii urease: purification, characterization, and
RT isolation of gene sequences.";
RL J. Bacteriol. 172:3073-3080(1990).
CC -1- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
CC -1- SUBUNIT: (ALPHA, BETA, GAMMA) (3) (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE UREASE GAMMA SUBUNIT FAMILY.
DR PIR; C35389; C35389.
KW Hydrolase.
FT NON_TER
SQ SEQUENCE 10 AA; 1171 MW; 4B313BCB077771A7 CRC64;

Query Match 24.6%; Score 14; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRVY 7
DB 5 PPEVK 10

RESULT 10
BPP_AGKHP STANDARD; PRT; 11 AA.
AC P04562;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting
DE enzyme inhibitor).
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydinus halys

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OS pallas).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidostauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Gloydius.
 OX NCBI_TaxID=8714;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA MEDLINE=86177022; PubMed=3008123;
 RT Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.,
 "Structure-function studies on the bradykinin potentiating peptide
 from Chinese snake venom (Agkistrodon halys pallas).";
 RL Peptides 6 Suppl. 3:339-342(1985).
 CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
 ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
 BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
 CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
 DR PIR: J0C002; XAVIBH.
 KM Hypotensive agent; Venom.
 FT MOD.RES
 SQ SEQUENCE 11 AA; 1112 MW; 30BAFF1277686777 CRC64;
 Query Match 24.6%; Score 14; DB 1; Length 11;
 Best Local Similarity 50.0%; Pred. No. 6.3e+03;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 1 GPRV 4
 DB 6 GPPI 9
 RESULT 11
 MORN_HUMAN STANDARD; PRT; 11 AA.
 ID MORN_HUMAN
 AC P01163;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Morphogenetic neuropeptide (Head activator) (HA).
 OS Homo sapiens (Human).
 OS Rattus norvegicus (Rat).
 OS Bos taurus (Bovine).
 OS Anthopleura elegantissima (Sea anemone), and
 OS Hydra attenuata (Hydra) (Hydra vulgaris).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Primates; Carnivora; Homiidae; Homo.
 OX NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Human, Rat, and Bovine;
 RX MEDLINE=82035850; PubMed=7290191;
 RA Bodenmuller H., Schaller H.C.;
 RT "Conserved amino acid sequence of a neuropeptide, the head activator,
 from coelenterates to humans.";
 RL Nature 293:579-580(1981).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=A.elegantisima, and H.attenuata;
 RA Schaller H.C., Bodenmuller H.;
 RT "Isolation and amino acid sequence of a morphogenetic peptide from
 hydra.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).
 RN [3]
 RP SYNTHESIS.
 RX MEDLINE=82050803; PubMed=7297679;
 RA Bitt C., Zachmann B., Bodenmuller H., Schaller H.C.;
 RT "Synthesis of a new neuropeptide, the head activator from hydra.";
 RL FEBS Lett. 131:317-321(1981).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=90059923; PubMed=2583101;
 RA Schaller H.C., Druffel-Augustin S., Dubel S.;
 RT "Head activator acts as an autocrine growth factor for NH15-CA2 cells

RT in the G2/mitosis transition.";
 RL EMBO J. 8:3311-3318(1989).
 CC -1- FUNCTION: HA ACTS AS AN AUTOCRINE GROWTH FACTOR FOR NEURAL CELLS
 CC IN THE G2/MITOSIS TRANSITION.
 CC -1- CAUTION: THIS PEPTIDE WAS FIRST ISOLATED FROM NERVE CELLS OF HYDRA
 CC AND WAS CALLED HEAD ACTIVATOR BY THE AUTHORS, BECAUSE IT INDUCED
 CC HEAD-SPECIFIC GROWTH AND DIFFERENTIATION IN THIS ANIMAL. IT HAS
 CC BEEN FOUND IN MAMMALIAN INTESTINE AND HYPOTHALAMUS.
 DR PIR: B01427; YHNU.
 DR PIR: A01427; YHRT.
 DR PIR: C01427; YHBO.
 DR PIR: A93900; YHXA.
 DR PIR: B93900; YHJPHV.
 KM Growth factor; Cell cycle; Mitosis.
 FT MOD.RES
 SQ SEQUENCE 11 AA; 1142 MW; 37927417C325B878 CRC64;
 Query Match 24.6%; Score 14; DB 1; Length 11;
 Best Local Similarity 40.0%; Pred. No. 6.3e+03;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 OY 1 GPRV 5
 DB 5 GSKVI 9
 RESULT 12
 MNPI_LEPDE STANDARD; PRT; 7 AA.
 ID MNPI_LEPDE
 AC P42984;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Myotropic neuropeptide 1 (Lep-MNP-1).
 OS Lepitnotarsa decemlineata (Colorado potato beetle).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
 OC Cuculiformia; Phryganeae; Chrysomelidae; Chrysomelidae;
 OC Chrysomelinae; Lepitnotarsa.
 OX NCBI_TaxID=7539;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Head;
 RX MEDLINE=95380343; PubMed=7651886;
 RA Spittaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
 RA Grauwels L., van Leuven F., de Loof A.;
 RT "Identification, characterization, and immunological localization of
 RT a novel myotropic neuropeptide in the Colorado potato beetle,
 RT Lepitnotarsa decemlineata.";
 RL Peptides 16:365-374(1995).
 CC -1- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
 CC OVIDUCT.
 KM Neuropeptide; Amidation.
 FT MOD.RES
 SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;
 Query Match 22.8%; Score 13; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GP 2
 DB 4 GP 5
 RESULT 13
 UH11_RAT STANDARD; PRT; 7 AA.
 ID UH11_RAT
 AC P56576;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Unknown protein from 2D-page of heart tissue (Spot P11) (Fragment).

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Wistar; TISSUE=Heart;
 RA L. X.-P., Pleissner K.-P., Schejter C., Regitz-Zagrosek V., Salikov J.,
 RA Jungblut P.R.;
 RL Submitted (SEP-1998) to the SWISS-PROT data bank.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 8.5, ITS MW IS: 42 kDa.
 CC UNSURE
 FT NON TER 7 7
 FT 7 7
 SQ SEQUENCE 7 AA; 775 MW; 6866DB040DC5A60 CRC64;

Query Match 22.8%; Score 13; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 QSA 11
 DB 1 QSA 3

RESULT 14
 AL15_CARMA STANDARD; PRT; 8 AA.
 ID AL15_CARMA
 AC P81819;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinus statin 15.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 OC Brachyura; Eubrachyura; Portunidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 CC Neuropeptide; Amidation; Multigene family.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD RES 8
 FT 8
 SQ SEQUENCE 8 AA; 811 MW; 922879D5AB47687D CRC64;

Query Match 22.8%; Score 13; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GP 2
 DB 2 GP 3

RESULT 15
 AL16_CARMA STANDARD; PRT; 8 AA.
 ID AL16_CARMA
 AC P81819;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinus statin 16.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;

OC Brachyura; Eubrachyura; Portunidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 CC Neuropeptide; Amidation; Multigene family.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD RES 8
 FT 8
 SQ SEQUENCE 8 AA; 813 MW; 7C286B45AB476878 CRC64;

Query Match 22.8%; Score 13; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GP 2
 DB 2 GP 3

Search completed: June 27, 2003, 17:33:31
 Job time : 23 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 17:19:12 ; Search time 77 Seconds
(without alignments)
29.435 Million cell updates/sec

Title: US-10-019-439-1
Perfect score: 57
Sequence: 1 GPRVRRHQSA 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1588

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirts:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	36.8	8	10	Q42507 triticum ae
2	20	35.1	8	13	P79940 xenopus lae
3	20	35.1	9	6	Q9T777 bos taurus
4	18	31.6	8	6	Q9GMH3 lagomorhyn
5	18	31.6	8	6	Q28866 megastera n
6	18	31.6	9	6	Q9GUV3 lagomorhyn
7	18	31.6	9	6	Q9GUV2 lagomorhyn
8	18	31.6	9	6	Q9GUV1 lagomorhyn
9	18	31.6	10	2	Q8RUF1 lagomorhyn
10	17	29.8	8	5	Q02032 lytechinus
11	17	29.8	9	2	Q9R7H9 haemophilus
12	17	29.8	9	2	P82568 streptococc
13	17	29.8	9	11	Q99MG3 mus muscul
14	17	29.8	10	5	Q93LX4 vldrio chol
15	17	29.8	10	5	P82222 bombyx mori
16	17	29.8	11	2	P71228 escherichia

17	16	28.1	9	3	Q9UR18	Q9ur18 sclerotium
18	16	28.1	10	2	Q9S3J6	Q9s3j6 escherichia
19	16	28.1	11	5	P82699	P82699 leucophaea
20	16	28.1	11	5	P82700	P82700 leucophaea
21	16	28.1	11	6	Q9GL48	Q9gl48 sus scrofa
22	16	28.1	11	6	Q9S083	Q9s083 leucana se
23	15	26.3	7	15	Q07624	Q07624 rous sarcom
24	15	26.3	8	2	Q9R7T2	Q9r7t2 escherichia
25	15	26.3	8	12	Q84156	Q84156 orf virus (
26	15	26.3	9	2	Q45533	Q45533 bacillus su
27	15	26.3	9	5	Q9TW6	Q9tw6 leptinocars
28	15	26.3	9	11	Q8R514	Q8r514 rattus norv
29	15	26.3	10	2	Q8VN85	Q8vn85 helicobacte
30	15	26.3	10	4	Q9UNF2	Q9unf2 homo sapien
31	15	26.3	10	4	Q96019	Q96019 homo sapien
32	15	26.3	10	8	Q9T2P3	Q9t2p3 rattus sp.
33	15	26.3	11	15	Q83410	Q83410 mouse mamma
34	14	24.6	8	2	Q45889	Q45889 clostridium
35	14	24.6	8	4	Q15894	Q15894 homo sapien
36	14	24.6	8	8	Q9GD47	Q9gd47 hydra staele
37	14	24.6	8	8	Q9GC24	Q9gc24 nenga pumil
38	14	24.6	9	2	Q9R7E8	Q9r7e8 escherichia
39	14	24.6	9	4	Q9H326	Q9h326 homo sapien
40	14	24.6	9	8	Q9GD12	Q9gd12 linospadix
41	14	24.6	9	8	Q9GCV6	Q9gcv6 sclerosperm
42	14	24.6	9	12	Q84333	Q84333 simian viru
43	14	24.6	10	2	Q9R7J8	Q9r7j8 helicobacte
44	14	24.6	10	11	Q9QVK7	Q9qvk7 mus sp. mep
45	14	24.6	10	12	Q84140	Q84140 influenzavi

ALIGNMENTS

RESULT 1
ID Q42507 PRELIMINARY; PRT; 8 AA.

AC Q42507;
DT 01-NOV-1996 (TREMURel. 01, Created)
DT 01-NOV-1996 (TREMURel. 01, Last sequence update)
DT 01-NOV-1998 (TREMURel. 08, Last annotation update)
DE Heat shock protein (Fragment).
GN HSP70C OR HSP70A OR HSP70B.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV MISTANG;
RX MEDLINE=96189275; PubMed=8605312;
RA Joshi C.P., Kumar S., Nguyen H.T.;
RT "Application of modified differential display technique for cloning
RT and sequencing of the 3' region from three putative members of wheat
RT HSP70 gene family.";
RL Plant Mol. Biol. 30:641-646(1996).
DR EMBL; L41507; AAB02333.1; -;
DR EMBL; L41505; AAB02331.1; -;
DR EMBL; L41506; AAB02332.1; -;
KW Heat shock.
FT NON TER 1
SQ SEQUENCE 8 AA; 866 MW; 71B2CB1B10532768 CRC64;

Query Match 36.8%; Score 21; DB 10; Length 8;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPRVRE 6
DB 1 GPRVRE 6

RESULT 2
 P79940 PRELIMINARY; PRT; 8 AA.
 AC P79940;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE XMeisl-4 protein (Fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97202105; PubMed=9049632;
 RA Steelman S., Moskow J.J., Muzynski K., North C., Druck T.,
 RA Montgomery J.C., Huebner K., Daar I.O., Buchberg A.M.;
 RT "Identification of a conserved family of Meisl-related homeobox
 genes."
 RT Genome Res. 7:142-156 (1997).
 DR EMBL; U68389; AAB19199.1; -.
 DR TRANSFAC; T03410; -.
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA; 1187 MW; 278B51F37B11F40B CRC64;

Query Match 35.1%; Score 20; DB 13; Length 8;
 Best Local Similarity 75.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 ERHQ 9
 DB 1 ERHE 4
 RESULT 3
 Q9TT77 PRELIMINARY; PRT; 9 AA.
 AC Q9TT77;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Wilm's tumor protein 1 (Fragment).
 GN WTL.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21015404; PubMed=11130975;
 RA Brouillette J.A., Andrew J.R., Venta P.J.;
 RT "Estimate of nucleotide diversity in dogs with a pool-and-sequence
 method."
 RT Mamm. Genome 11:1079-1086 (2000).
 DR EMBL; AF202074; AAF20919.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 9 AA; 1231 MW; 58DDF41A16D1F403 CRC64;

Query Match 35.1%; Score 20; DB 6; Length 9;
 Best Local Similarity 60.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 VERHO 9
 DB 1 LKRHQ 5
 RESULT 4
 Q9GMH3 PRELIMINARY; PRT; 8 AA.
 ID Q9GMH3

AC Q9GMH3;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE Actin (Fragment).
 OS Lagenorhynchus obscurus (Dusky dolphin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
 OC Lagenorhynchus.
 NCBI_TaxID=27611;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hare M.P., Cipriano F., Palumbi S.R.;
 RT "Slow Evolution of Genetic Monophyly in Dolphins: Implications for
 Speciation, Systematics and Conservation."
 RT Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF140833; AAF98686.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA; 962 MW; 5BD1F417740862C0 CRC64;

Query Match 31.6%; Score 18; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 RHQ 9
 DB 4 RHQ 6
 RESULT 5
 Q28866 PRELIMINARY; PRT; 8 AA.
 AC Q28866;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE Actin protein (Fragment).
 GN ACTIN.
 OS Megaptera novaeangliae (Humpback whale).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
 OC Balaeopteridae; Megaptera.
 NCBI_TaxID=9773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94285813; PubMed=7912407;
 RA Palumbi S.R., Baker C.S.;
 RT "Contrasting population structure from nuclear intron sequences and
 mtDNA of humpback whales."
 RT Mol. Biol. Evol. 11:426-435 (1994).
 DR EMBL; S73467; AAD14118.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA; 906 MW; 69C866D1F4177408 CRC64;

Query Match 31.6%; Score 18; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 RHQ 9
 DB 4 RHQ 6
 RESULT 6
 Q9GUV3 PRELIMINARY; PRT; 9 AA.
 ID Q9GUV3;
 AC Q9GUV3;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE Actin (Fragment).
 OS Lagenorhynchus obscurus (Dusky dolphin).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Lagomorhynchus.
OX NCBI_TaxID=27611;
RN [1]
RP SEQUENCE FROM N.A.
RA Hare M.P., Cipriano F., Palumbi S.R.;
RT "Slow Evolution of Genetic Monophyly in Dolphins: Implications for
RT Speciation, Systematics and Conservation."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF140834; AAF98687.1; -
DR EMBL; AF140832; AAF98685.1; -
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 9 AA; 1049 MW; 1D0EF417740862C0 CRC64;

Query Match 31.6%; Score 18; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RHQ 9
Db 7 RHQ 9

RESULT 7
Q9GJV2 PRELIMINARY; PRT; 9 AA.
ID Q9GJV2
AC Q9GJV2;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE Actin (Fragment).
OS Lagomorhynchus obliquidens (Pacific white-sided dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Lagomorhynchus.
OX NCBI_TaxID=90247;
RN [1]
RP SEQUENCE FROM N.A.
RA Hare M.P., Cipriano F., Palumbi S.R.;
RT "Slow Evolution of Genetic Monophyly in Dolphins: Implications for
RT Speciation, Systematics and Conservation."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF140831; AAF98684.1; -
DR EMBL; AF140827; AAF98680.1; -
DR EMBL; AF140828; AAF98681.1; -
DR EMBL; AF140829; AAF98682.1; -
DR EMBL; AF140830; AAF98683.1; -
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 9 AA; 1049 MW; 1D0EF417740862C0 CRC64;

Query Match 31.6%; Score 18; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RHQ 9
Db 7 RHQ 9

RESULT 8
Q9GJV1 PRELIMINARY; PRT; 9 AA.
ID Q9GJV1
AC Q9GJV1;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE Actin (Fragment).
OS Lagomorhynchus acutus (Atlantic white-sided dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Lagomorhynchus.
OX NCBI_TaxID=90246;
RN [1]
RP SEQUENCE FROM N.A.
RA Hare M.P., Cipriano F., Palumbi S.R.;
RT "Slow Evolution of Genetic Monophyly in Dolphins: Implications for
RT Speciation, Systematics and Conservation."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF140825; AAF98678.1; -
DR EMBL; AF140822; AAF98675.1; -
DR EMBL; AF140823; AAF98676.1; -
DR EMBL; AF140824; AAF98677.1; -
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 9 AA; 1049 MW; 1D0EF417740862C0 CRC64;

Query Match 31.6%; Score 18; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 RHQ 9
Db 7 RHQ 9

RESULT 9
Q8RUF1 PRELIMINARY; PRT; 10 AA.
ID Q8RUF1
AC Q8RUF1;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE Porin-like protein (Fragment).
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=NC16-2, TC29-5, AND TC97;
RC TRANSPOSON=TN5041A1, TN5041B, AND TN5041D1;
RA Kholidi G.Y., Gorienco Z.M., Mandlin S.Z., Nikiforov V.G.;
RT "Distribution of distinct microvariants of TN5041 in environmental
RT bacteria."
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ422128; CAD19527.1; -
DR EMBL; AJ422129; CAD19528.1; -
DR EMBL; AJ422130; CAD19529.1; -
FT NON TER 10
FT NON TER 10
SQ SEQUENCE 10 AA; 1206 MW; 23C47E7401F5A417 CRC64;

Query Match 31.6%; Score 18; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPR 3
Db 2 GPR 4

RESULT 10
O02032 PRELIMINARY; PRT; 8 AA.
ID O02032
AC O02032;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE Metallothionein (Fragment).
GN LMT2.
OS Lytechinus pictus (Painted sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Echinozoa; Echinodermata; Echinozoa; Echinozoa; Echinozoa;

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OC Lytechinus.
 OX NCBI_TaxID=7653;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97264487; PubMed=9110313;
 RA Cserjesi P., Fang H., Brandhorst B.P.;
 RT "Metallothionein gene expression in embryos of the sea urchin
 Lytechinus pictus.";
 RL Mol. Reprod. Dev. 47:39-46(1997).
 DR EMBL; U03400; AAB58320.1; -.
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 823 MW; EBD5A2C1F7686766 CRC64;

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 Best Local Similarity 75.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GPRV 4
 DB 3 GPHV 6

RESULT 11

ID Q9R7H9 PRELIMINARY; PRT; 9 AA.
 AC Q9R7H9;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Lipoprotein (Fragment).
 GN NLPD.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 CC Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96083063; PubMed=9422600;
 RA Martin K., Morlin G., Smith A., Nordyke A., Eisenstark A., Golomb M.;
 RT "The typhophanase gene cluster of Haemophilus influenzae type b:
 RT evidence for horizontal gene transfer.";
 RL J. Bacteriol. 180:107-118(1998).
 DR EMBL; AF003252; AAB96582.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 9 AA; 1152 MW; 35A017673B4412D7 CRC64;

Query Match 29.8%; Score 17; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 RVERH 8
 DB 4 RYLPRH 9

RESULT 12

ID P82568 PRELIMINARY; PRT; 9 AA.
 AC P82568;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE Unknown protein from 2D-page (Fragment).
 GN Streptococcus pyogenes.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 CC Streptococcaceae; Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC STRAIN=JRS4;
 RA Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W., Rogers J.,
 RA Vanbogelen R.A.;
 RT "Two-dimensional gel electrophoresis map of Streptococcus pyogenes

RT proteins.";
 RL Submitted (MAY-2000) to the SWISS-PROT data bank.
 CC -1- MASS SPECTROMETRY: MW=22592.04; METHOD=ELECTROSPRAY.
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1069 MW; 2A771042CB1AB2D7 CRC64;

Query Match 29.8%; Score 17; DB 2; Length 9;
 Best Local Similarity 75.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 VVER 7
 DB 6 VIER 9

RESULT 13

ID Q99MG3 PRELIMINARY; PRT; 9 AA.
 AC Q99MG3;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE NRCAM protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA More M.I., Kirsch F.P., Rathjen F.G.;
 RT "Targeted ablation of NRCAM and ankyrin-B results in disorganized lens
 RT fibres leading to cataract formation.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF346472; AAK25814.1; -.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1039 MW; 32FCB721E333327 CRC64;

Query Match 29.8%; Score 17; DB 11; Length 9;
 Best Local Similarity 50.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 6 ERHQA 11
 DB 4 KKHLSA 9

RESULT 14

ID Q93LX4 PRELIMINARY; PRT; 10 AA.
 AC Q93LX4;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE MIOC (Fragment).
 GN MIOC.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O395;
 RA Saha A., Hareialka S., Bhadra R.K.;
 RT "Cloning and characterization of the origin of replication of
 RT chromosome 1 of Vibrio cholerae.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY034431; AAK61370.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 10 AA; 1303 MW; 464F014042D40337 CRC64;

Query Match 29.8%; Score 17; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 9.1e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RVER 7
 Db 5 RVINR 9

RESULT 15

P82222 PRELIMINARY; PRT; 10 AA.
 ID P82222
 AC P82222;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Unknown protein from 2D-page (Fragment).
 OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Bombycoidea; Bombycidae; Bombyx.
 ON NCBI_taxid=7091;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=XINHANG X KEMING; TISSUE=BODY WALL, AND FAT BODY;
 RX MEDLINE=21177481; PubMed=11280994;
 RA Zhong B.X.;
 RT "Protein database for several tissues derived from five instar of
 RT silkworm.";
 RL I Chuan Hsueh Pao 28:217-224(2001).
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1131 MW; 62CD783729D1B2CB CRC64;

Query Match 29.8%; Score 17; DB 5; Length 10;
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QY 1 GPRV 4
 Db 1 GPEV 4

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 Job time : 80 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 17:18:42 ; Search time 69 Seconds

(without alignments)
21.243 Million cell updates/sec

Title: US-10-019-439-1

Sequence: 1 GPRVRRHQSA 11

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Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 190898

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-Processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	11	22	ABR6978
2	53	93.0	10	16	AAW1132
3	41	71.9	10	19	AAW6536
4	36	63.2	7	8	AAW71315
5	36	63.2	7	11	AAW6526
6	36	63.2	8	15	AAW65794
7	31	54.4	6	21	AAW01536
8	31	54.4	6	23	AAW8565
9	29.5	51.8	9	20	AAW92903
10	29	50.9	9	22	AAW82729

11	29	50.9	9	22	AAW02382
12	27	47.4	5	17	AAW96173
13	27	47.4	5	12	ABP12165
14	27	47.4	9	22	ABP20324
15	27	47.4	10	22	ABP12325
16	27	47.4	10	22	ABP18613
17	26	45.6	5	17	AAW96189
18	26	45.6	5	17	AAW96146
19	26	45.6	7	17	AAW96188
20	26	45.6	8	17	AAW96187
21	26	45.6	9	23	ABG35045
22	26	45.6	10	23	AAW96186
23	26	45.6	10	17	AAW95341
24	25	43.9	9	23	AAW49396
25	25	43.9	9	23	AAW94685
26	25	43.9	9	23	AAW94915
27	25	43.9	9	23	AAW95033
28	25	43.9	10	21	AAW27523
29	25	43.9	10	23	AAW94589
30	25	43.9	10	23	AAW94769
31	25	43.9	10	23	AAW95352
32	25	43.9	10	23	AAW95433
33	24	42.1	8	22	ABP14283
34	24	42.1	8	22	ABP20219
35	24	42.1	8	22	ABP22541
36	24	42.1	8	22	ABP67361
37	24	42.1	9	22	ABP12166
38	24	42.1	9	22	ABP20082
39	24	42.1	9	22	AAW99127
40	24	42.1	9	22	AAW83144
41	24	42.1	10	22	ABP12326
42	24	42.1	10	22	ABP18549
43	24	42.1	10	22	AAW99128
44	24	42.1	10	23	AAW49611
45	24	42.1	11	21	AAW15868

ALIGNMENTS

RESULT 1
ABR6978
ID ABR6978 standard; peptide; 11 AA.
AC ABR6978;
DT 22-JUL-2002 (first entry)
DE Residues 36-46 of human fibrinogen alpha chain precursor.
DS Anti-arthritis; anti-inflammatory; fibrin; rheumatoid polyarthritis;
KW human; fibrinogen alpha chain.
OS Homo sapiens.
XX FR2795735-A1.
XX 05-JAN-2001.
XX 01-JUL-1999; 99FR-0008470.
XX PF 01-JUL-1999; 99FR-0008470.
XX PR 01-JUL-1999; 99FR-0008470.
XX (UYTO-) UNIV TOULOUSE SABATIER PAUL.
XX Serre G, Sebba M;
XX WPI; 2001-114394/13.
PT New citrulline-containing polypeptide from fibrin, useful for diagnosis
PS and treatment of rheumatoid polyarthritis
XX Example 1; Page 11; 23pp; French.

XX The present invention relates to a citrulline (Cit) containing
 CC polypeptide derived from all or part of the alpha- or beta-chains of
 CC fibrin by substitution of at least one arginine residue by Cit. The Cit
 CC containing polypeptides can be used for in vitro diagnosis of rheumatoid
 CC polyarthritis (RP), by detecting disease-specific autoantibodies, and
 CC therapeutically for neutralising the RP-associated autoimmune response.
 CC The present sequence is a fragment (residues 36-46) of the human
 CC fibrinogen alpha chain precursor, which was used in an example from the
 CC invention.
 XX
 SQ Sequence 11 AA;
 Query Match 100.0%; Score 57; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 GPRVERHQA 11
 Db 1 GPRVERHQA 11
 RESULT 2
 AAW11932
 ID AAW11932 standard; peptide, 10 AA.
 XX
 AC AAW11932;
 XX
 DT 02-APR-1997 (first entry)
 XX
 DE Fibrinogen B-beta-chain residues 15-24.
 XX
 KM Monoclonal; antibody; human; soluble; fibrin; fibrinogen;
 KM urea-treated; des-AAB; B-beta-chain; immunoassay; diagnosis;
 KM disseminated intravascular coagulation.
 XX
 OS Homo sapiens.
 XX
 PN W09512617-A1.
 XX
 PD 11-MAY-1995.
 XX
 PF 01-NOV-1994; 94WO-JP01844.
 XX
 PR 02-NOV-1993; 93JP-0297325.
 XX
 PA (IATR) IATRON LAB INC.
 XX
 PI Inuzuka K, Ito Y, Kohno I, Soe G;
 XX
 DR WPI; 1995-206667/27.
 XX
 PT Monoclonal antibody reactive with soluble human fibrin - but not
 PT with fibrinogen, is useful for fibrin immunoassay in plasma
 PT specimens
 XX
 PS Example 3; Page 15; 32pp; Japanese.
 XX
 CC A novel monoclonal antibody (Mab) reacts with human soluble fibrin,
 CC but not with human fibrinogen. Specifically when the Mab reacts
 CC with urea-treated des-AAB fibrin the reaction is not inhibited by
 CC peptides corresponding to fibrinogen A-alpha-chain residues 17-26
 CC (AAW11931), B-beta-chain residues 15-24 (AAW11932) or gamma-chain
 CC residues 312-324 (AAW11933). The Mab is useful in immunoassays for
 CC soluble fibrin in plasma samples (e.g. by sandwich immunoassay),
 CC particularly for the diagnosis of pathological conditions such as
 CC disseminated intravascular coagulation.
 CC
 SO Sequence 10 AA;
 Query Match 93.0%; Score 53; DB 16; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00079;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GPRVERHQA 10
 Db 1 GPRVERHQA 10
 RESULT 3
 AAW65536
 ID AAW65536 standard; peptide, 10 AA.
 XX
 AC AAW65536;
 XX
 DT 12-OCT-1998 (first entry)
 XX
 DE Biotinyl-fibrin-anti-polymerant peptide.
 XX
 KM Endothelin-1; angiotensin II receptor; imaging; cardiovascular disease;
 KM losartan; contrast medium; diagnosis; lanthanide; biotin;
 KM fibrin-anti-polymerant peptide.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FH Modified-site 1
 FT Modified-site /note="biotinylated Gly"
 FT Modified-site 10
 FT Modified-site /note="C-terminal amide"
 XX
 PN W09818496-A2.
 XX
 PD 07-MAY-1998.
 XX
 PF 28-OCT-1997; 97WO-GB02956.
 XX
 PR 24-MAR-1997; 97GB-0006063.
 PR 28-OCT-1996; 96GB-0022364.
 PR 28-OCT-1996; 96GB-0022365.
 PR 28-OCT-1996; 96GB-0022366.
 PR 28-OCT-1996; 96GB-0022367.
 PR 28-OCT-1996; 96GB-0022368.
 PR 28-OCT-1996; 96GB-0022369.
 PR 15-JAN-1997; 97GB-0000699.
 PR 04-FEB-1997; 97GB-0002195.
 XX
 PA (COCK) COCKBAIN J.
 PA (NYCO-) NYCOMED IMAGING AS.
 XX
 PI Cutbertson A, Klavens J, Naevestad A;
 XX
 DR WPI; 1998-348067/30.
 XX
 PT New angiotensin II receptor binding compounds - useful for imaging
 PT cardiovascular diseases and disorders
 XX
 PS Example 10; Page 88; 99pp; English.
 XX
 CC The invention relates to organic compounds of formula V-L-R, V = organic
 CC group having binding affinity for an angiotensin II receptor site; L = a
 CC linker group or a bond; R = a group detectable in vivo imaging of a
 CC human or animal body; provided that when V is angiotensin or a peptidic
 CC angiotensin derivative or analogue, then V-L-R is not a non-metal
 CC radionuclide substituted peptide and L-V is not simply a peptide with a
 CC chelating agent amide bonded to a side chain. Also claimed are: (1) 123I-
 CC losartan and 131I-losartan; (2) the use of the organic compound for the
 CC manufacture of a contrast medium for use in diagnosis involving
 CC administration of the contrast medium to an animate subject and
 CC generating an image of at least part of the subject; (3) a method of
 CC contrast agent comprising the organic compound and generating an image
 CC of at least part of the subject and (4) a method of monitoring the
 CC effect of treatment of animals with a drug to combat or provoke effects
 CC associated with angiotensin II comprising administration of the organic
 CC compound and detecting the uptake of the agent by angiotensin II

CC receptors, the administration and detection being optionally (and
CC preferably) effected repeatedly. The organic compounds are useful for
CC imaging cardiovascular diseases and disorders. The present sequence
CC represents biocinyl-fibrin-anti-polymerant peptide.

XX
SQ Sequence 10 AA;

Query Match 71.9%; Score 41; DB 19; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.18;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPRVRRHOS 10
DB 1 GPRPERRHOS 10

RESULT 4
AAP71315

ID AAP71315 standard; peptide; 7 AA.

XX AAP71315;

DT 03-OCT-2002 (updated)

DT 19-JUN-1991 (first entry)

XX Sequence of fibrin immunogen for the prepn. of monoclonal antibodies
DE (MAbs).

XX Fibrin-specific monoclonal antibody; screening.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 7 /label= Arg-OH

XX W08706263-A.

XX 22-OCT-1987.

PF 14-APR-1987; 87MO-US00862.

PR 14-APR-1986; 86US-0851514.

XX (GEHO-) GEN HOSPITAL CORP.

PA (GENO-) GEN HOSPITAL CORP.

XX Matsueda GR, Haber E;

XX WPI; 1987-306855/43.

PT Screening of fibrin-specific monoclonal antibodies - by contact
PT with immobilised crosslinked fibrin clot and screening with
PT detectable labelling step

XX Disclosure; Page 7; 41pp; English.

XX The MAbs are specific to fibrin without fibrinogen cross-reactivity.
CC They have increased binding to in vitro and in vivo thrombi. The
CC MAbs can be used in immunoassays for fibrin in the presence of
CC fibrinogen or other proteins. They can be used as immunoaffinity
CC ligands for the purification of fibrin.
CC (updated on 03-OCT-2002 to add missing OS field.)

XX Sequence 7 AA;

Query Match 63.2%; Score 36; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRVRR 7
DB 1 GPRVRR 7

RESULT 5
AAR06526
ID AAR06526 standard; protein; 7 AA.

XX AAR06526;

DT 11-OCT-1990 (first entry)

DE Peptide antigenic to fibrin.

XX fibrin, fibrinogen; thrombi; immunoaffinity.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 2 /label=His or Pro

FT Misc-difference 4 /label=Pro or Val

FT Misc-difference 5 /label=Leu or Val

FT Misc-difference 6 /label=Asp or Glu

FT Misc-difference 7 /label=Lys or Arg

XX US4927916-A.

XX 22-MAY-1990.

PF 30-JAN-1986; 86US-0824228.

PR 23-APR-1984; 84US-0603155.

PR 30-JAN-1986; 86US-0824228.

XX (GEHO-) GEN HOSPITAL CORP.

XX Matsueda GR, Haber E, Hui K;

XX WPI; 1990-185723/24.

PT Fibrin-specific monoclonal antibodies -

PT lacking fibrinogen cross-reactivity, obtd. using peptide(s)

XX comprising fibrin-specific epitopic sequences.

XX Claim 1; Page 17; 12pp; English.

XX Peptide is epitopic to fibrin, allowing anti-fibrin Abs to be
CC raised without cross-reactivity to fibrinogen. They are
CC particularly useful in detection of fibrin and thrombi.

XX Sequence 7 AA;

Query Match 63.2%; Score 36; DB 11; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRVRR 7
DB 1 GPRVRR 7

RESULT 6
AAR65794

ID AAR65794 standard; peptide; 8 AA.

XX AAR65794;

DT 26-JUN-1995 (first entry)

XX Fibrin-specific epitopic peptide.

XX Fibrin-specific epitopic peptides; thrombi detection; fibrinogen;
 KW antifibrin-specific monoclonal antibodies.
 XX Synthetic.
 OS
 XX US5357042-A.
 PN
 XX 18-OCT-1994.
 PD
 XX 23-APR-1984; 84US-0603155.
 PF
 XX 23-APR-1984; 84US-0603155.
 PR 23-APR-1984; 84US-0603155.
 PR 30-JAN-1986; 86US-0824228.
 PR 22-DEC-1989; 89US-0454954.
 PR 24-AUG-1992; 92US-0932729.
 XX
 XX (GEMO) GEN HOSPITAL CORP.
 PA
 XX Haber E, Matsueda GR;
 PI
 XX WPI; 1994-33241/41.
 DR
 XX Synthetic epitopic peptide(s) of variable length - capable of
 PT eliciting fibrin specific antibodies free of fibrinogen
 PT cross-reactivity.
 XX
 XX Example 9; Column 14; 12pp; English.
 PS
 XX AAR65789-665794 are synthetic peptides comprising fibrin-specific
 CC epitopic sequences, they can be used to prepare hybridoma cell
 CC lines, which produce antifibrin-specific monoclonal antibodies
 CC substantially devoid of fibrinogen cross-reactivity. These
 CC antibodies are useful in the in vivo and in vitro detection
 CC of thrombi and fibrin deposits.
 XX
 SQ Sequence 8 AA;
 Query Match 63.2%; Score 36; DB 15; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRVVER 7
 Db 1 GPRVVER 7

RESULT 7
 AAB01536
 ID AAB01536 standard; peptide; 6 AA.
 XX
 AC AAB01536;
 XX
 DT 08-NOV-2000 (first entry)
 XX
 DE Plasmin substrate site found in fibrinogen.
 XX
 KW Polymer; biomaterial; conjugate; hydrogel; drug delivery; adhesive;
 KW sealant; tissue engineering; wound healing; scaffold;
 KW cell transplant; adhesion prevention; cell migration; collagenase;
 KW plasmin; elastase.
 XX
 OS Synthetic.
 OS
 XX WO200044808-A1.
 PN
 XX 03-AUG-2000.
 PD
 XX 01-FEB-2000; 2000WO-US02608.
 PF
 XX 01-FEB-1999; 99US-0118093;
 PR
 XX (HUBB/) HUBBELL J A.
 PA

XX Hubbell JA, Elbert D, Luitolf M, Pratt A, Schoenmakers R;
 PI Tirelli N, Vernon B;
 PI
 XX WPI; 2000-524289/47.
 DR
 XX Producing polymeric biomaterials by polymerizing two or more precursor
 FT components (e.g. polymer, protein or peptide) of the biomaterial,
 FT useful for delivering therapeutic molecules to a subject and as
 PT adhesives or sealants
 XX
 PS Disclosure; Page 44; 11pp; English.
 XX
 XX A method of making polymeric biomaterials is described comprising
 CC combining two or more precursor components (e.g. polymer, protein or
 CC peptide) of the biomaterial under conditions that allow
 CC polymerisation of the two components. Polymerisation occurs through
 CC self selective reaction between a strong nucleophile and a conjugated
 CC unsaturated bond or a conjugated unsaturated group, by nucleophilic
 CC addition. The polymeric hydrogels can be used in a variety of
 CC applications. They can be used to deliver therapeutic molecules to
 CC a subject, as adhesives or sealants (e.g. sealing air leaks on the
 CC lung), as tissue engineering and wound healing scaffolds, and as cell
 CC transplant devices. The biomaterials are also useful for adhesion
 CC prevention to minimise unwanted operative or post-traumatic adhesions.
 CC In the instances where the precursor for the polymeric biomaterial
 CC is a peptide, the nucleophile is the amino acid cysteine. This
 CC results in peptides of structure similar to H-2N-CXXXXCXXXXC-COOH
 CC (see GENESEQ records AAB01531-B01535). The length of XXXXX is variable
 CC and can be of any number. It is particularly useful when the
 CC sequences in the domains shown as XXXXX are substrates for enzymes
 CC that are involved in cell migration (e.g. as substrates for enzymes
 CC such as collagenase, plasmin or elastase).
 XX
 SQ Sequence 6 AA;
 Query Match 54.4%; Score 31; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPRVVE 6
 Db 1 GPRVVE 6

RESULT 8
 AA085665
 ID AA085665 standard; Peptide; 6 AA.
 XX
 AC AA085665;
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DE Plasmin substrate site found in fibrin #1.
 XX
 KW Biomaterial; vasotrophic; anticoagulant; thrombolytic;
 KW vulnery; infection; adhesion; thrombosis; restenosis; adhesive;
 KW sealant; tissue engineering; wound healing scaffold;
 KW cell transplant device.
 XX
 OS Unspecified.
 OS
 XX WO200192584-A1.
 PN
 XX 06-DEC-2001.
 PD
 XX 04-JUN-2001; 2001WO-US18101.
 PF
 XX 02-JUN-2000; 2000US-0586937.
 PR
 XX (EIDG-) EIDGENOESSISCHE TECH HOCHSCHULE ZUERICH.
 PA (UTZU-) UNIV ZURICH.
 XX

PI Hubbel JA, Elbert D, Schoenmakers R;
XX
XX WPI; 2002-205802/26.
XX
PT New biomaterial useful for medical treatment comprises an active or a
PT binding group and has an ester or amide bond onto the active or binding
PT group -
XX
XX Disclosure; Page 81; 222pp; English.
XX
XX The invention relates to a biomaterial comprising an active or a binding
CC group and has an ester or amide bond onto the active or binding group.
CC Also included is a biomaterial (II) formed from the cross-linking of at
CC least two precursor components of formula D-Y-C(O)-(CH₂)₂-n-S-(CH₂)₂-
CC -COX-P', D-Y-C(O)-(CH₂)₂-n-NH-(CH₂)₂-2-COX-P', D-Y-C(O)-(CH₂)₂-n-NH-U-P,
CC D-Y-C(O)-(CH₂)₂-n-S-U-P', D-Y-C(O)-(CH₂)₂-n-S-L-S-CH₂-2-CO-X-P',
CC D-Y-C(O)-(CH₂)₂-n-S-L-S-U-P', D-Y-C(O)-(CH₂)₂-n-NH-L-S-CH₂-2-CO-X-P',
CC D-Y-C(O)-(CH₂)₂-n-NH-L-S-U-P', D-Y-C(O)-(CH₂)₂-n-S-L-NH-CH₂-2-CO-X-
CC -CO-X-P', or D-Y-C(O)-(CH₂)₂-n-NH-L-NH-U-P'. The half-life of the ester
CC or amide bond onto the active or binding group is 1 hour - 1 year in an
CC aqueous solution at pH 7.4 and 37 plusOC. Forming (II) involves
CC (a) attaching the active or binding compound to the linker molecule or
CC incorporating a nucleophilic amine or thiol into the active or binding
CC compound, (b) removing any thiol- or amine-protecting groups in the
CC linker (c) coupling a thiol, amine or alkene in the linker or
CC incorporated into the active or binding compound to the water soluble or
CC water swellable polymer containing conjugated unsaturated groups by a
CC conjugate addition reaction to form a precursor component and
CC (d) cross-linking the uncoupled conjugated unsaturated groups in at
CC least one precursor component. D = active or binding group; Y = O, NH or
CC N; L = linear or branched linker; X = O or N; P' = water-soluble or water
CC -swellable polymer containing conjugated unsaturated groups;
CC U = product of the addition of a nucleophile to an electrophile that
CC is attached to the water-soluble or water-swellable polymer; and
CC n = 2 - 3. The biomaterials are useful for treating or preventing
CC disease, disorder or infection in a mammal e.g. human, for preventing
CC adhesions, thrombosis or restenosis in a mammal and for delivering the
CC active compound (preferably protein or peptide) to a cell, tissue, organ,
CC organ system or a body of a mammal as adhesives or sealants, as tissue
CC engineering and wound healing scaffolds and as cell transplant devices.
CC The bond of the biomaterial has a half life of 1 hour - 1 year
CC (preferably 1 day - 9 months, especially 2 days - 2 months) in an aqueous
CC solution at pH 7.4 and 37plusOC. Thus the biomaterial releases the
CC therapeutic compound over a clinically relevant time-frame. The
CC present sequence is a peptide which acts as a therapeutically
CC active compound suitable for inclusion in the biomaterial of the
CC invention.
XX
XX
SQ Sequence 6 AA;
Query Match 54.4%; Score 31; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPRVVE 6
| | | | |
| | | | |
Db 1 GPRVVE 6
RESULT 9
AAW92903
ID AAW92903 standard; peptide; 9 AA.
XX
XX AAW92903;
AC
XX
XX 14-MAY-1999 (first entry)
DT
XX
XX Fibrinogen ligand peptide #7.
DE
XX
XX Fibrinogen; ligand; fibrin; treatment; prevention; rheology; diabetes;
KW microcirculatory disorder; retinopathy; polynuropathy; apoplexy; sepsis;
KW hearing loss; sepsis; occlusive arterial disease; kidney function.

XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 9 /note="C-terminal amidated"
FT
FT
XX
XX WO9902565-A2.
XX
XX 21-JAN-1999.
PD
XX
XX 02-JUL-1998; 98WO-EP04090.
PF
XX
XX 10-JUL-1997; 97DE-1029591.
PR
XX
XX (THER-) THERASORB MEDIZINISCHE SYSTEME GMBH.
PA
XX
XX Bieber F, Koll R, Richter W, Tschoepe W;
PI
PI WPI; 1999-120788/10.
DR
XX
XX Using ligand for fibrinogen or fibrin to treat or prevent
PT microcirculatory disorders - and to control blood rheology, e.g.
PT diabetes-related conditions, also adsorb material with bound
PT ligand for the process
XX
XX Disclosure; Page 17; 23pp; German.
XX
XX This invention describes the use of a ligand for fibrinogen and/or fibrin
CC for preparation of an agent for treating or preventing microcirculatory
CC disorders and/or for modifying rheology, in mammals. The products of the
CC invention can be specifically used to treat or prevent disorders
CC associated with diabetes, retinopathy, polynuropathy, apoplexy, hearing
CC loss, sepsis, occlusive arterial disease and/or impaired kidney function
CC Reducing the amount of fibrinogen and/or fibrin in the blood alleviates
CC disease symptoms.
XX
XX
SQ Sequence 9 AA;
Query Match 51.8%; Score 29.5; DB 20; Length 9;
Best Local Similarity 70.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 1 GPRVVERHOS 10
| | | | |
| | | | |
Db 1 GPR-PEHRS 9
RESULT 10
AAB82729
ID AAB82729 standard; Peptide; 9 AA.
XX
XX AAB82729;
AC
XX
XX 29-OCT-2001 (first entry)
DT
XX
XX Factor VIII:C B domain C-terminal peptide.
DE
XX
XX Factor VIII:C; human; haemophilia A; blood clotting; therapy;
KW diagnosis.
KW
XX
XX Homo sapiens.
OS
XX
XX US2001016340-A1.
PN
XX
XX 23-AUG-2001.
PD
XX
XX 22-DEC-2000; 2000US-0748062.
PF
XX
XX 03-DEC-1993; 93US-0161770.
PR
PR 07-FEB-1991; 91US-0652099.
PR 16-MAY-1995; 95US-0441943.
PR 27-JAN-1986; 86US-0822989.

PR 19-MAY-1987; 87US-0051916.
 XX
 XX (CHIR) CHIRON CORP.
 PA (NOVO) NOVO NORDISK AS.
 XX
 XX Chapman B, Burke RL, Rasmussen ME, Mikkelsen JM;
 XX WPI; 2001-535541/59.
 DR
 XX
 PT New polypeptide having Factor VIII:C activity, for treating classical
 PT (Type A) haemophilia and other blood clotting disorders, for use as
 PT immunogens for producing antibodies, or for use in diagnostic assays
 PT for Factor VIII:C.
 XX
 XX Claim 12; Page 27; 29pp; English.
 XX
 CC The present sequence is that of the C-terminal sequence of the
 CC B domain of human Factor VIII:C. The invention relates to
 CC recombinant protein complexes having Factor VIII:C activity,
 CC and methods for their production in eukaryotic host cells. The
 CC recombinant protein complexes comprise a first polypeptide
 CC homologous to human Factor VIII:C A domain and a second polypeptide
 CC homologous to human Factor VIII:C C domain. The first polypeptide
 CC may be extended at its C-terminal end by a B domain sequence
 CC comprising the N-terminal sequence of human Factor VIII:C B domain
 CC (see AAB82727), a hinge peptide (see AAB82728) homologous to a
 CC human immunoglobulin heavy chain hinge region, and the B domain
 CC C-terminus (present sequence). The protein complexes are useful for
 CC treating classical (Type A) haemophilia and other blood clotting
 CC disorders. They are also useful as immunogens for producing
 CC antibodies, for isolating von Willebrand factor by affinity
 CC chromatography, or in diagnostic assays for Factor VIII:C.
 XX
 SQ Sequence 9 AA:
 Query Match 50.9%; Score 29; DB 22; Length 9;
 Best Local Similarity 62.5%; Pred. No. 7.8e+05;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 PVERRHQ 9
 | : : : :
 Db 1 PVLKRHQ 8
 RESULT 11
 ID AAE02382
 XX AAE02382 standard; peptide; 9 AA.
 AC AAE02382;
 XX
 DT 10-AUG-2001 (first entry)
 XX
 DE Human Factor VIII:C B-domain C-terminal sequence.
 XX
 KW Human; Factor VIII:C; FVIII:C; coagulation; von-Willebrand factor;
 KW type A haemophilia; blood clotting disorder; haemostatic; gene therapy;
 KW recombinant protein; immunogen.
 XX
 OS Homo sapiens.
 XX
 PN US6228620-B1.
 XX
 PD 08-MAY-2001.
 XX
 PF 16-MAY-1995; 95US-0441943.
 XX
 PR 03-DEC-1993; 93US-0161770.
 PR 07-FEB-1991; 91US-0652099.
 PR 27-JAN-1986; 86US-0822989.
 PR 19-MAY-1987; 87US-0051916.
 XX
 XX (CHIR) CHIRON CORP.
 PA (NOVO) NOVO NORDISK AS.

XX
 PT Chapman B, Burke RL, Rasmussen ME, Mikkelsen JM;
 XX WPI; 2001-335014/35.
 DR
 XX
 PT New nucleic acid complexes having factor VIII activity and coagulation
 PT activity, for treating hemophilia and other blood clotting disorders,
 PT or as immunogens for the production of antibodies.
 XX
 XX Example 7; Column 51-52; 33pp; English.
 XX
 CC The patent relates to a nucleic acid composition for introducing
 CC nucleic acid into a eukaryotic host cell to obtain expression of a
 CC recombinant protein which lacks all or a portion of the B domain of
 CC human Factor VIII:C (hFVIII:C) and is capable of coagulation activity.
 CC The recombinant protein consists of a polypeptide substantially
 CC homologous to mature A domain of hFVIII:C as encoded by the
 CC polynucleotide present in plasmid pSVF8-200 (ATCC number 40190); and
 CC a second polypeptide homologous to mature C domain of hFVIII:C as
 CC encoded by the polynucleotide present in plasmid pSVF8-200.
 CC The composition is useful as an immunogen for the production of
 CC antibodies, for isolating von-Willebrand factor by affinity
 CC chromatography, in diagnostic assays for Factor VIII:C and for treating
 CC Type A haemophilia and other blood clotting disorders.
 CC The present sequence is C-terminal fragment of human Factor VIII:C
 CC B-domain used in the recombinant protein of the invention.
 XX
 SQ Sequence 9 AA:
 Query Match 50.9%; Score 29; DB 22; Length 9;
 Best Local Similarity 62.5%; Pred. No. 7.8e+05;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 PVERRHQ 9
 | : : : :
 Db 1 PVLKRHQ 8
 RESULT 12
 ID AAR96173
 XX AAR96173 standard; peptide; 5 AA.
 AC AAR96173;
 XX
 DT 19-DEC-1996 (first entry)
 XX
 DE Fibrinogen epitope, represents alpha chain residues 22-26.
 XX
 KW Epitope; cleavage product; human; leukocyte elastase; HLE; fibrinogen;
 KW monoclonal antibody; probe; detection; antigen; blood; peritoneal fluid;
 KW sputum; bronchoalveolar lavage fluid; assay; inhibitor; arthritis;
 KW pulmonary emphysema; chronic bronchitis; cystic fibrosis; bronchiectasis;
 KW chronic obstructive pulmonary disease; myelogenous leukaemia;
 KW infantile respiratory distress syndrome; gout;
 KW adult respiratory distress syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO9614580-A1.
 XX
 PD 17-MAY-1996.
 XX
 PF 03-NOV-1995; 95WO-US13794.
 XX
 PR 06-JUN-1995; 95US-0469141.
 PR 07-NOV-1994; 94US-0335524.
 PA (MERI) MERCK & CO INC.
 XX
 PT Boger JS, Dahlgren ME, Davies DTP, Humes JL, Mumford RA;
 XX WPI; 1996-251888/25.
 DR
 XX

PT New isolated fibrinogen derived cleavage products - used for
 PT detection of leukocyte elastase activity in disease diagnosis and
 PT for evaluating elastase inhibitors
 XX
 PS Disclosure; Page 21; 109pp; English.

CC The sequences given in AAR96164-81 represent antigenic peptides derived
 CC from the N-terminus of the primary cleavage products of human leukocyte
 CC elastase (HLE) cleaved human fibrinogen. These epitopes are capable
 CC of inducing specific antibodies and acting as specific probes for
 CC the detection of antibodies. Monoclonal antibodies reactive against
 CC these peptides, and other HLE cleaved fibrinogen derived peptides (see
 CC also AAR96146-63 and AAR96182-94) are prepared by standard techniques.
 CC These monospecific antibodies may be used to assay for the formation
 CC of complementary cleavage product antigens or epitopes in whole blood
 CC or other body fluids, peritoneal fluid, sputum or bronchoalveolar
 CC lavage fluid. The assay for cleavage products is dependent upon the
 CC presence of HLE in the sample. This assay can also be used for the
 CC evaluation of HLE inhibitors. The antibodies may be used to diagnose
 CC and monitor diseases such as arthritis, gout, pulmonary emphysema,
 CC chronic bronchitis, cystic fibrosis, chronic obstructive pulmonary
 CC disease, bronchiectasis, adult or infantile respiratory distress
 CC syndrome and myelogenous leukaemia.

SQ Sequence 5 AA;
 XX

Query Match 47.4%; Score 27; DB 17; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ERHQS 10
 DB 1 ERHQS 5

RESULT 13
 ABP12165
 ID ABP12165 standard; Peptide; 9 AA.
 XX
 AC ABP12165;
 XX
 DT 15-JUL-2002 (first entry)
 DE HIV A02 super motif env peptide #222.
 XX
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpr; vif; tat; cytoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO200124810-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US27766.
 XX
 PR 05-OCT-1999; 99US-0412863.
 XX
 PA (EPTM-) EPIMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Cells E, Kubo RT, Grey HM,
 XX
 DR WPI; 2001-354887/37.
 XX
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -
 XX
 PS Claim 32; Page 118; 448pp; English.
 XX
 CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid

CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigen is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines.
 CC An additional advantage of an group-based vaccine approach is the ability
 CC to combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention.

SQ Sequence 9 AA;
 XX

Query Match 47.4%; Score 27; DB 22; Length 9;
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RYVERHQS 11
 DB 1 RYVEREKRA 9

RESULT 14
 ABP20224
 ID ABP20224 standard; Peptide; 9 AA.
 XX
 AC ABP20224;
 XX
 DT 15-JUL-2002 (first entry)
 DE HIV A03 motif env peptide #428.
 XX
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
 KW vpr; vif; tat; cytoxic T lymphocyte; CTL; immune response; epitope;
 KW antigen; vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO200124810-A1.
 XX
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US27766.
 XX
 PR 05-OCT-1999; 99US-0412863.
 XX
 PA (EPTM-) EPIMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Cells E, Kubo RT, Grey HM,
 XX
 DR WPI; 2001-354887/37.
 XX
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1 -
 XX
 PS Claim 32; Page 284; 448pp; English.
 XX
 CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I)
 CC may be used for immunising subjects against HIV-1 infections. The use of

group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABL1501 to ABLP5412 represent peptide sequences used in the exemplification of the present invention.

Sequence 9 AA;

Query Match 47.4%; Score 27; DB 22; Length 9;
Best Local Similarity 66.7%; Pred. No. 7.8e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0.

3 RVERHQA 11
||| | | | | |
1 RVEREKRA 9

RESULT 15
ABP12325
ABP12325 standard; Peptide; 10 AA.
XX
AC ABP12325;
XX
DT 15-JUL-2002 (first entry)
XX
DE HIV A02 super motif env peptide #382.
XX
KM HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
KW vif; tat; cytoxic T lymphocyte; CTL; immune response; epitope;
KM antigen; vaccine; HIV infection; immunisation; vitucide.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000WO-US27766.
XX
PR 05-OCT-1999; 99US-0412863.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
PI WPI; 2001-354887/37.
XX
DR

Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 -

Claim 32; Page 121; 448pp; English.

The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABP25347 to ABP25397). (I) has vitucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole

CC antigen is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines.
CC An additional advantage of an group-based vaccine approach is the ability
CC to combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP11501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention.

XX

Sequence	10 AA;
Query Match	47.4%;
Best Local Similarity	66.7%; Pred. No. 1e+02;
Matches	6; Conservative 1; Mismatches 2; Indels 0; Gaps 0

Qy 3 RVERHOSA 11
 ||||| :
Db 1 RVEREKKA 9

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Search completed: June 27, 2003, 17:31:38
Job time : 71 secs
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GenCore version 5.1.6
Copyright (c) 1993 -.2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 27, 2003, 17:33:38 ; Search time 48 Seconds
(without alignments)
25.127 Million cell updates/sec

Title: US-10-019-439-1
Perfect score: 57
Sequence: 1 GRRVERHQSA 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 424699 seqs, 109646833 residues

Total number of hits satisfying chosen parameters: 61044

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep.*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
10: /cgn2_6/ptodata/1/pubpaa/US05_PUBCOMB pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	78.9	9	10	US-09-953-657-5
2	41	71.9	10	10	US-09-765-614B-10
3	41	71.9	10	10	US-09-925-715-7
4	29	50.9	9	10	US-09-748-062-34
5	28	49.1	10	9	US-10-062-710-91
6	26	45.6	10	9	US-10-309-851-28
7	25	43.9	10	9	US-10-228-806-63
8	24	42.1	7	9	US-09-954-385-26
9	23	40.4	10	9	US-10-328-806-62
10	23	40.4	10	9	US-09-865-548A-180
11	22	38.6	9	9	US-09-922-405B-23
12	22	38.6	9	9	US-10-066-474-23
13	22	38.6	10	8	US-08-424-550B-278
14	22	38.6	11	10	US-09-291-809C-9
15	22	38.6	11	10	US-09-845-849-9
16	21	36.8	6	9	US-10-058-513-26
17	21	36.8	7	9	US-09-903-185-4
18	21	36.8	8	9	US-10-185-425-21
19	21	36.8	8	9	US-09-876-904A-188

20	21	36.8	8	10	US-09-243-079-49	Sequence 49, Appl
21	21	36.8	9	9	US-09-799-250-28	Sequence 28, Appl
22	21	36.8	9	9	US-09-799-250-58	Sequence 58, Appl
23	21	36.8	9	9	US-09-799-250-161	Sequence 161, Appl
24	21	36.8	9	9	US-09-799-250-350	Sequence 350, Appl
25	21	36.8	9	9	US-09-799-250-451	Sequence 451, Appl
26	21	36.8	9	9	US-09-799-250-547	Sequence 547, Appl
27	21	36.8	9	9	US-09-799-250-661	Sequence 661, Appl
28	21	36.8	10	9	US-09-799-250-69	Sequence 69, Appl
29	21	36.8	10	9	US-09-799-250-482	Sequence 482, Appl
30	21	36.8	10	9	US-09-799-250-596	Sequence 596, Appl
31	21	36.8	10	9	US-09-799-250-603	Sequence 603, Appl
32	21	36.8	10	9	US-09-799-250-703	Sequence 703, Appl
33	21	36.8	10	10	US-09-824-568-5	Sequence 5, Appl
34	21	36.8	11	10	US-09-976-165-54	Sequence 54, Appl
35	20	35.1	7	9	US-09-884-767A-12	Sequence 12, Appl
36	20	35.1	8	9	US-09-876-904A-524	Sequence 524, Appl
37	20	35.1	8	9	US-09-876-904A-525	Sequence 525, Appl
38	20	35.1	8	10	US-09-243-079-47	Sequence 47, Appl
39	20	35.1	8	10	US-09-243-079-48	Sequence 48, Appl
40	20	35.1	9	9	US-10-125-635A-60	Sequence 60, Appl
41	20	35.1	9	9	US-10-125-635A-136	Sequence 136, Appl
42	20	35.1	9	9	US-10-125-635A-193	Sequence 193, Appl
43	20	35.1	9	9	US-09-938-864-60	Sequence 60, Appl
44	20	35.1	9	9	US-09-938-864-136	Sequence 136, Appl
45	20	35.1	9	9	US-09-938-864-193	Sequence 193, Appl

ALIGNMENTS

RESULT 1

US-09-953-657-5
GENERAL INFORMATION:

APPLICANT: Buettner, Joseph A.
Dadd, Christopher A.
Baumbach, George A.
Hammond, David J.

TITLE OF INVENTION: Fibrinogen Binding Peptides

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSER: Bayer Corporation
STREET: 800 Dwight Way
P. O. Box 1986

CITY: Berkeley
STATE: California

COUNTRY: USA
ZIP: 94701-1986

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB Storage
COMPUTER: IBM

OPERATING SYSTEM: DOS
SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/953,657
FILING DATE: 17-Sep-2001

CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/595,718

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Gliblin, James A.

REGISTRATION NUMBER: 25772
REFERENCE/DOCKET NUMBER: MSB-7233

TELECOMMUNICATION INFORMATION:
TELEPHONE: (510)705-7910
TELEFAX: (510)705-7904

JOURNAL: Thromb. Haemost.
VOLUME: 63

ISSUE: 3
PAGES: 439-444

DATE: 28-JUN-1990

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-953-657-5

Query Match 78.9%; Score 45; DB 10; Length 9;
Best Local Similarity 88.9%; Pred. No. 3.8e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRVERHQ 9
1 GPRVERHQ 9
1 GPRVERHQ 9

US-09-765-614B-10

Sequence 10, Application US/09765614B
Patent No. US20020102215A1
GENERAL INFORMATION:

APPLICANT: Nycomed Imaging AS
TITLE OF INVENTION: Improvements in or relating to
TITLE OF INVENTION: diagnostic/therapeutic
FILE REFERENCE: REF/Klaveness/054
CURRENT APPLICATION NUMBER: US/09/765,614B
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 10
LENGTH: 10
TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial

OTHER INFORMATION: Sequence: Biotinylated

NAME/KEY: MOD_RES

LOCATION: (1)

OTHER INFORMATION: Biotinylated-Gly

NAME/KEY: MOD_RES

LOCATION: (10)

OTHER INFORMATION: AMIDATION

US-09-765-614B-10

US-09-925-715-7

Sequence 7, Application US/09925715
Patent No. US20020102217A1
GENERAL INFORMATION:

APPLICANT: Nycomed Imaging AS
TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
FILE REFERENCE: REF/Klaveness/206
CURRENT APPLICATION NUMBER: US/09/925,715
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 7
LENGTH: 10
TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Biotinylated

OTHER INFORMATION: fibrin-antipolymerant peptide

NAME/KEY: MOD_RES

LOCATION: (1)

OTHER INFORMATION: Biotin-Gly

NAME/KEY: MOD_RES

LOCATION: (10)

OTHER INFORMATION: AMIDATION

US-09-925-715-7

Query Match 71.9%; Score 41; DB 10; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPRVERHQ 10
1 GPRVERHQ 10
1 GPRVERHQ 10

US-09-748-062-34

Sequence 34, Application US/09748062
Patent No. US20010016340A1
GENERAL INFORMATION:

APPLICANT: CHAPMAN, BARBARA
BURKE, RAE LYNN
RASMUSSEN, MIRELLA EZBAN
MICKELSON, JAN MOLLER
TITLE OF INVENTION: PROTEIN COMPLEXES HAVING FACTOR VIII.C
ACTIVITY AND PRODUCTION THEREOF
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSER: REED & ROBINS
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/748,062
FILING DATE: 22-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/441,943
FILING DATE: <Unknown>
APPLICATION NUMBER: US 822,989
FILING DATE: 27-JAN-1986

ATTORNEY/AGENT INFORMATION:
NAME: BAROVSKY, KENNETH
REGISTRATION NUMBER: 36,442
REFERENCE/DOCKET NUMBER: 2300-0048.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3400

INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 34:

US-09-748-062-34

Query Match 50.9%; Score 29; DB 10; Length 9;
Best Local Similarity 62.5%; Pred. No. 3.8e+05;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PPRVERHQ 9
1 PPRVERHQ 9
1 PPRVERHQ 9

DB 1 PPRVERHQ 9

RESULT 5
US-10-062-710-91
; Sequence 91, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank Q.
; APPLICANT: Chu, Yong-Liang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; TITLE OF INVENTION: Via Peptide Vaccines
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; PRIOR FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV CTL-Epitopes
US-10-062-710-91

Query Match 49.1%; Score 28; DB 9; Length 10;
Best Local Similarity 62.5%; Pred. No. 44;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PRVERHQ 9
| | | | |
| | | | |
DB 1 PRVERHQ 8

RESULT 6
US-10-309-851-28
; Sequence 28, Application US/10309851
; Publication No. US20030108554A1
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; APPLICANT: Revert-Ros, Francisco
; TITLE OF INVENTION: G1Pe, a Family of Polypeptides with Transcription Factor Activity
; TITLE OF INVENTION: Interact with Goodpasture Antigen Binding Protein
; FILE REFERENCE: 98/723-F-US
; CURRENT APPLICATION NUMBER: US/10/309,851
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-851-28

Query Match 45.6%; Score 26; DB 9; Length 10;
Best Local Similarity 57.1%; Pred. No. 1e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 RYVERHQ 9
| | | | |
| | | | |
DB 3 KYVERKH 9

RESULT 7
US-10-228-806-63
; Sequence 63, Application US/10228806
; Publication No. US20030049237A1
; GENERAL INFORMATION:
; APPLICANT: Bannion, et al.
; TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reactions
; TITLE OF INVENTION: to Allergy
; FILE REFERENCE: 2002834-0043

; CURRENT APPLICATION NUMBER: US/10/228,806
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arachis hypogaea
US-10-228-806-63

Query Match 43.9%; Score 25; DB 9; Length 10;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GPRVERHQ 9
| | | | |
| | | | |
DB 2 GPRVERHQ 10

RESULT 8
US-09-954-385-26
; Sequence 26, Application US/09954385
; Publication No. US20030100467A1
; GENERAL INFORMATION:
; APPLICANT: Aehle, Wolfgang
; APPLICANT: Baldwin, Toby L.
; APPLICANT: Van Gastel, Franciscus J.C.
; APPLICANT: Janssen, Christelle G.
; APPLICANT: Murray, Christopher J.
; APPLICANT: Wang, Huaming
; APPLICANT: Winetzy, Deborah S.
; TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
; FILE REFERENCE: GC690
; CURRENT APPLICATION NUMBER: US/09/954,385
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: binding peptide
US-09-954-385-26

Query Match 42.1%; Score 24; DB 9; Length 7;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 VVERHOS 10
| | | | |
| | | | |
DB 1 LVNKHOS 7

RESULT 9
US-10-228-806-62
; Sequence 62, Application US/10228806
; Publication No. US20030049237A1
; GENERAL INFORMATION:
; APPLICANT: Bannion, et al.
; TITLE OF INVENTION: Methods and Reagents for Decreasing Clinical Reactions
; FILE REFERENCE: 2002834-0043
; CURRENT APPLICATION NUMBER: US/10/228,806
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arachis hypogaea
US-10-228-806-62

Query Match 40.4%; Score 23; DB 9; Length 10;
Best Local Similarity 71.4%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPRV 7
Db 4 GPRV 10

RESULT 10
US-09-865-548A-180

; Sequence 180, Application US/09865548A
; Publication No. US20030096298A1
; GENERAL INFORMATION:
; APPLICANT: Barnea, Elion
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamari
; APPLICANT: Admon, Ari
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 180
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-180

Query Match 40.4%; Score 23; DB 9; Length 10;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRV 5
Db 4 GPRV 8

RESULT 11

US-09-922-405B-23
; Sequence 23, Application US/09922405B
; Publication No. US20020182218A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles A.
; FILE OF INVENTION: THERAPEUTIC ANTI-MELANOMA COMPOUNDS
; FILE REFERENCE: G2 2103.00
; CURRENT APPLICATION NUMBER: US/09/922,405B
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/223,641
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/255,502
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 60/264,432
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/279,005
; PRIOR FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-922-405B-23

Query Match 38.6%; Score 22; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRV 4
Db 6 GPRV 9

RESULT 12
US-10-066-474-23

; Sequence 23, Application US/10066474
; Publication No. US20030013075A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles A.
; TITLE OF INVENTION: MART-1 COMPOUNDS FOR THERAPY AND
; FILE REFERENCE: G2 2103.20
; CURRENT APPLICATION NUMBER: US/10/066,474
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 09/922,405
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: US 60/223,641
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/255,502
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 60/264,432
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 60/279,005
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-066-474-23

Query Match 38.6%; Score 22; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRV 4
Db 6 GPRV 9

RESULT 13

US-08-424-550B-278
; Sequence 278, Application US/08424550B
; Patent No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMT J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHRHOF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/APeD
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 278:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-550B-278

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Query Match          38.6%; Score 22; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 5.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY      2 PRVVR 7
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Db      4 PRVVR 9

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RESULT 14
US-09-291-809C-9
; Sequence 9, Application US/09291809C
; Patent No. US20010049831A1
; GENERAL INFORMATION:
; APPLICANT: Detlef Weigel
; APPLICANT: Salk Institute
; TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
; TITLE OF INVENTION: MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT
; FILE REFERENCE: SALKINS.026CP1
; CURRENT APPLICATION NUMBER: US/09/291,809C
; CURRENT FILING DATE: 1999-04-14
; PRIOR APPLICATION NUMBER: PCT/US99/08151
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 09/060,726
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-291-809C-9

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Query Match          38.6%; Score 22; DB 10; Length 11;
Best Local Similarity 66.7%; Pred. No. 6.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY      1 GPRVVE 6
      |||:|
Db      4 GTRVIE 9

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RESULT 15
US-09-845-849-9
; Sequence 9, Application US/09845849
; Patent No. US20020029395A1
; GENERAL INFORMATION:
; APPLICANT: THE SALK INSTITUTE FOR BIOLOGICAL STUDIES
; APPLICANT: WEIGEL, Detlef
; APPLICANT: KARDAITSKY, Igor
; TITLE OF INVENTION: FLOWERING LOCUS T (FT) AND GENETICALLY
; TITLE OF INVENTION: MODIFIED PLANTS HAVING MODULATED FLOWER DEVELOPMENT

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; FILE REFERENCE: SALKINS.026DVI
; CURRENT APPLICATION NUMBER: US/09/845,849
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 09/060,726
; PRIOR FILING DATE: 1998-04-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-845-849-9

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```

Query Match          38.6%; Score 22; DB 10; Length 11;
Best Local Similarity 66.7%; Pred. No. 6.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY      1 GPRVVE 6
      |||:|
Db      4 GTRVIE 9

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Search completed: June 27, 2003, 17:42:48
Job time : 49 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 27, 2003, 17:30:27 ; Search time 26 Seconds
(without alignments)
12.448 Million cell updates/sec

Title: US-10-019-439-1

Perfect score: 57
Sequence: 1 GPRVVERHQA 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 83753

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/aa/5B_COMB.pep:*
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4: /cgn2_6/prodata/1/aa/5B_COMB.pep:*
5: /cgn2_6/prodata/1/aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	53.0	10	2	US-08-448-547-2
2	45	9	1	US-08-595-718A-5
3	41	10	4	US-08-960-054A-10
4	41	10	4	US-08-958-993A-10
5	41	10	4	US-08-959-206A-7
6	36	7	2	US-08-762-695-11
7	36	11	3	US-08-592-500-40
8	36	11	3	US-08-195-006-40
9	36	11	5	PCT-US94-07644A-40
10	31	8	3	US-08-434-099A-37
11	29	9	4	US-08-441-843-34
12	27	5	3	US-08-469-141A-33
13	27	5	3	PCT-US95-1379A-33
14	27	10	3	US-09-139-762A-74
15	26	5	3	US-08-469-141A-15
16	26	5	3	US-08-469-141A-51
17	26	5	3	US-08-469-141A-57
18	26	5	5	PCT-US95-1379A-15
19	26	5	5	PCT-US95-1379A-51
20	26	5	5	PCT-US95-1379A-57
21	26	7	3	US-08-469-141A-42
22	26	7	5	PCT-US95-1379A-42
23	26	7	5	PCT-US95-1379A-50
24	26	8	3	US-08-469-141A-49
25	26	8	5	PCT-US95-1379A-49
26	26	10	3	US-09-139-762A-95
27	26	10	3	US-08-469-141A-48

28	26	45.6	10	5	PCT-US95-1379A-48	Sequence 48, Appl
29	22	38.6	4	1	US-07-932-200-7	Sequence 7, Appl
30	22	38.6	4	2	US-08-387-749-7	Sequence 7, Appl
31	22	38.6	4	2	US-08-685-589A-36	Sequence 36, Appl
32	22	38.6	4	5	PCT-US93-08231-7	Sequence 7, Appl
33	22	38.6	6	3	US-08-856-074A-38	Sequence 38, Appl
34	22	38.6	7	6	5231168-13	Patent No. 5231168
35	22	38.6	8	4	US-08-444-818-517	Sequence 517, App
36	22	38.6	10	4	US-08-469-260A-278	Sequence 278, App
37	22	38.6	11	3	US-08-856-074A-37	Sequence 37, App
38	22	38.6	11	3	US-08-592-500-39	Sequence 39, Appl
39	22	38.6	11	3	US-08-195-006-39	Sequence 39, Appl
40	22	38.6	11	4	US-09-060-726A-9	Sequence 9, Appl
41	22	38.6	11	5	PCT-US94-07644A-39	Sequence 39, Appl
42	21	36.8	4	2	US-08-685-589A-35	Sequence 35, Appl
43	21	36.8	7	2	US-08-713-298B-4	Sequence 4, Appl
44	21	36.8	7	2	US-08-870-180B-4	Sequence 4, Appl
45	21	36.8	7	4	US-09-226-529-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-448-547-2
; Sequence 2, Application US/08448547
; Patent No. 5821068
; GENERAL INFORMATION:
; APPLICANT: Soe, Gilbu
; APPLICANT: Kohno, Isao
; APPLICANT: Inuzuka, Kimiko
; APPLICANT: Ito, Yumiko
; TITLE OF INVENTION: ANTI-HUMAN SOLUBLE FIBRIN ANTIBODY,
; TITLE OF INVENTION: HYBRIDOMA, AND IMMUNOASSAYING METHOD
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSER: SUGHRUE, MIOW, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,547
; FILING DATE: 30-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/01844
; FILING DATE: 01-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-297325
; FILING DATE: 02-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: Q-38931
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-448-547-2

Query Match 93.0%; Score 53; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRVERHOS 10
DB 1 GPRVERHOS 10

RESULT 2

US-08-595-718A-5
Sequence 5, Application US/08595718A
Patent No. 5723579
GENERAL INFORMATION:
APPLICANT: Buettner, Joseph A.
APPLICANT: Dadd, Christopher A.
APPLICANT: Hammond, David J.
TITLE OF INVENTION: Fibrinogen Binding Peptides
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bayer Corporation
STREET: 800 Dwight Way
STREET: P. O. Box 1986
CITY: Berkeley
STATE: California
COUNTRY: USA
ZIP: 94701-1986
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB Storage
COMPUTER: IBM
OPERATING SYSTEM: DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,718A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Giblin, James A.
REGISTRATION NUMBER: 25772
REFERENCE/DOCKET NUMBER: MSB-7233
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510)705-7910
TELEFAX: (510)705-7904
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: single strand
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: peptide
PUBLICATION INFORMATION:
AUTHORS: Kuyas, C.
AUTHORS: Haeblerli, A.
AUTHORS: Walder, P.
AUTHORS: Straub, P. W.
TITLE: Isolation of Human Fibrinogen and its
TITLE: Derivatives by Affinity Chromatography on Gly-Pro-
TITLE: Arg-Pro-Lys-Fractogel
JOURNAL: Thromb. Haemost.
VOLUME: 63
ISSUE: 3
PAGES: 439-444
DATE: 28-JUN-1990
US-08-595-718A-5

Query Match 78.9%; Score 45; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.9e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRVERHQ 9
DB 1 GPRVERHK 9

RESULT 3

US-08-960-054A-10
Sequence 10, Application US/08960054A
Patent No. 6261537
GENERAL INFORMATION:
APPLICANT: Nycomed Imaging AS
TITLE OF INVENTION: Improvements in or relating to
diagnostic/therapeutic
TITLE OF INVENTION: agents
FILE REFERENCE: REF/Klaveness/054
CURRENT APPLICATION NUMBER: US/08/960,054A
CURRENT FILING DATE: 1997-10-29
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial
OTHER INFORMATION: Sequence: Biotinylated
OTHER INFORMATION: fibrin-anti-polymerant peptide
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: Biotinylated-Gly
NAME/KEY: MOD_RES
LOCATION: (10)
OTHER INFORMATION: AMIDATION
US-08-960-054A-10

Query Match 71.9%; Score 41; DB 4; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.054;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPRVERHOS 10
DB 1 GPRPPERHOS 10

RESULT 4

US-08-958-993A-10
Sequence 10, Application US/08958993A
Patent No. 6264917
GENERAL INFORMATION:
APPLICANT: Nycomed Imaging AS
TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
TITLE OF INVENTION: agents
FILE REFERENCE: REF/Klaveness/993
CURRENT APPLICATION NUMBER: US/08/958,993A
CURRENT FILING DATE: 1997-10-28
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Biotinylated
OTHER INFORMATION: fibrin-anti-polymerant peptide
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: Biotinylated-Gly
NAME/KEY: MOD_RES
LOCATION: (10)
OTHER INFORMATION: AMIDATION
US-08-958-993A-10

Query Match 71.9%; Score 41; DB 4; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.054;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPRVRRHOS 10
DB 1 GPRVRRHOS 10

RESULT 5

US-08-959-206A-7
Sequence 7, Application US/08959206A
Patent No. 6331289
GENERAL INFORMATION:
APPLICANT: Nycomed Imaging AS
TITLE OF INVENTION: Improvements in or relating to diagnostic/therapeutic
FILE REFERENCE: REF/Klaavness/206
CURRENT APPLICATION NUMBER: US/08/959,206A
CURRENT FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Biotinylated,
OTHER INFORMATION: fibrin-antipolymerant peptide
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: Biotin-Gly
NAME/KEY: MOD_RES
LOCATION: (10)
OTHER INFORMATION: AMIDATION
US-08-959-206A-7

Query Match 71.9%; Score 41; DB 4; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.054;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPRVRRHOS 10
DB 1 GPRVRRHOS 10

RESULT 6

US-08-762-695-11
Sequence 11, Application US/08762695
Patent No. 5846738
GENERAL INFORMATION:
APPLICANT: SEIDEL, CHRISTOPH
APPLICANT: BIALK, PETER
APPLICANT: VON DER ELTZ, HERBERT
TITLE OF INVENTION: SYNTHETIC STANDARD FOR IMMUNOASSAYS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIKO, MARMELESTEIN, MURRAY, AND ORAM
STREET: METROPOLITAN SQUARE, 655 15TH ST, N.W., SUITE
STREET: 330-G ST. LOBBY
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,695
FILING DATE: 12-DEC-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/325,589
FILING DATE: 19-OCT-1994
APPLICATION NUMBER: DE P 43 35 798.9
FILING DATE: 20-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 17 735.6
FILING DATE: 20-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 20 742.5
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: NOLAN, SHARON L.
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P1614.4050
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-762-695-11

Query Match 63.2%; Score 36; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRVRR 7
DB 1 GPRVRR 7

RESULT 7

US-08-592-500-40
Sequence 40, Application US/08592500
Patent No. 6005089
GENERAL INFORMATION:
APPLICANT: Lanza, Francois
APPLICANT: Phillips, David R.
APPLICANT: Cazenave, Jean-Pierre
TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,500
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,455
FILING DATE: 09-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 12418-28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 40:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..11
OTHER INFORMATION: /note="Amino acid sequence of the
OTHER INFORMATION: human fibrinogen (Fg) A-alpha 2 chain thrombin
OTHER INFORMATION: cleavage site."
FEATURE:
NAME/KEY: Region
LOCATION: 5..7
OTHER INFORMATION: /note="Amino acid residues
OTHER INFORMATION: identical to GPV."
US-08-592-500-40

Query Match 63.2%; Score 36; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRVER 7
Db 5 GPRVER 11

RESULT 8
US-08-195-006-40
Sequence 40, Application US/08195006
Patent No. 6083688
GENERAL INFORMATION:
APPLICANT: Lanza, Francois
APPLICANT: Phillips, David R.
APPLICANT: Cazenave, Jean-Pierre
TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,006
FILING DATE: 10-FEB-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,455
FILING DATE: 09-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 12418-28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Peptide

LOCATION: 1..11
OTHER INFORMATION: /note="Amino acid sequence of the
OTHER INFORMATION: human fibrinogen (Fg) A-alpha 2 chain thrombin
OTHER INFORMATION: cleavage site."
FEATURE:
NAME/KEY: Region
LOCATION: 5..7
OTHER INFORMATION: /note="Amino acid residues
OTHER INFORMATION: identical to GPV."
US-08-195-006-40

Query Match 63.2%; Score 36; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRVER 7
Db 5 GPRVER 11

RESULT 9
PCT-US94-07644A-40
Sequence 40, Application PC/TUS9407644A
GENERAL INFORMATION:
APPLICANT: COR Therapeutics, Inc.
TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07644A
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 012418-003000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..11
OTHER INFORMATION: /note="Amino acid sequence of the
OTHER INFORMATION: human fibrinogen (Fg) A-alpha 2 chain thrombin
OTHER INFORMATION: cleavage site."
FEATURE:
NAME/KEY: Region
LOCATION: 5..7
OTHER INFORMATION: /note="Amino acid residues
OTHER INFORMATION: identical to GPV."
PCT-US94-07644A-40

Query Match 63.2%; Score 36; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRVFR 7
DB 5 GPRVFR 11

RESULT 10

US-08-434-099A-37
Sequence 37, Application US/08434099A
Patent No. 6083902
GENERAL INFORMATION:
APPLICANT: Cederholm-Wms., Stewart A.
TITLE OF INVENTION: Recombinant Fibrin Chains,
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.R. Squibb & Sons, Inc.
STREET: 100 Headquarters Park Drive
CITY: Skillman
STATE: NJ
COUNTRY: USA
ZIP: 08558
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,099A
FILING DATE: 03-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,979
FILING DATE: 02-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Furman, Jr., Esq., Theodore R
REGISTRATION NUMBER: 30,942
REFERENCE/DOCKET NUMBER: CV00544
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-281-2372
TELEFAX: 908-281-2373
TELEX:
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-434-099A-37

Query Match 54.4%; Score 31; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRVFR 6
DB 3 GPRVFR 8

RESULT 11
US-08-441-943-34
Sequence 34, Application US/08441943
Patent No. 6228620
GENERAL INFORMATION:
APPLICANT: CHAPMAN, BARBARA
APPLICANT: BURKE, RAE LYNN
APPLICANT: RASMUSSEN, MIRELLA EZBAN
APPLICANT: MIKELSON, JAN MOLLER
TITLE OF INVENTION: PROTEIN COMPLEXES HAVING FACTOR VIII:C
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 285 HAMILTON AVENUE, SUITE 200

CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,943
FILING DATE: 16-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 051,916
FILING DATE: 19-MAY-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,989
FILING DATE: 27-JAN-1986
ATTORNEY/AGENT INFORMATION:
NAME: BAROVSKY, KENNETH
REGISTRATION NUMBER: 36,442
REFERENCE/DOCKET NUMBER: 2300-0048.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-441-943-34

Query Match 50.9%; Score 29; DB 4; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.9e+05;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 PRVFRHQ 9
DB 1 PVLKRHQ 8

RESULT 12
US-08-469-141A-33
Sequence 33, Application US/08469141A
Patent No. 6124107
GENERAL INFORMATION:
APPLICANT: MUMFORD, RICHARD A.
APPLICANT: DAVIES, D.T. PHILIP
APPLICANT: DAHLGREN, MARY E.
APPLICANT: BOGER, JOSHUA S.
TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: DR. CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE., P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,141A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 174611B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)-594-6734
TELEFAX: (908)-594-4720
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-469-141A-33

Query Match 47.4%; Score 27; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 6 ERHQS 10
Db 1 ERHQS 5

RESULT 13
PCT-US95-13794-33
Sequence 33, Application PC/TUS9513794
GENERAL INFORMATION:
APPLICANT: Mumford, Richard A.
APPLICANT: Davies, D.T. Philip
APPLICANT: Dahlgren, Mary E.
APPLICANT: Boger, Joshua S.
APPLICANT: Humes, John L.
TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
TITLE OF INVENTION: POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Dr. Christine E. Carty
STREET: 126 E. Lincoln Avenue; P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13794
FILING DATE: 03-NOV-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Carty, Christine E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 174611AY
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4720
TELEFAX: (908) 594-6734
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal

PCT-US95-13794-33

Query Match 47.4%; Score 27; DB 5; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 ERHQS 10
Db 1 ERHQS 5

RESULT 14

US-09-139-762A-74
Sequence 74, Application US/09139762A
Patent No. 6013453
GENERAL INFORMATION:
APPLICANT: Choo, Yen
APPLICANT: Klug, Aaron
APPLICANT: Sanchez Garcia, Isidro
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,762A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/793,408
FILING DATE: 02-JUN-1997
APPLICATION NUMBER: PCT/GB95/01949
FILING DATE: 17-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9514698.1
FILING DATE: 18-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9422534.9
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9416880.4
FILING DATE: 20-AUG-1994
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULAR TYPE: peptide
US-09-139-762A-74

Query Match 47.4%; Score 27; DB 3; Length 10;
Best Local Similarity 57.1%; Pred. No. 28;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 3 RYVERHQ 9
Db 3 RLDRHQ 9

RESULT 15
US-08-469-141A-15
Sequence 15, Application US/08469141A

Patent No. 6124107
GENERAL INFORMATION:
APPLICANT: MUMFORD, RICHARD A.
APPLICANT: DAVIES, D.T. PHILIP
APPLICANT: DAHLGREN, MARY E.
APPLICANT: BOGER, JOSHUA S.
APPLICANT: HUMES, JOHN L.
TITLE OF INVENTION: ASSAY FOR MARKER OF HUMAN
TITLE OF INVENTION: POLYMORPHONUCLEAR LEUKOCYTE ELASTASE ACTIVITY
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: DR. CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE, P.O. BOX 2000
CITY: RAHWAY
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,141A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 36,099
REFERENCE/DOCKET NUMBER: 174611B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)-594-4720
TELEFAX: (908)-594-6734
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-469-141A-15

Query Match 45.6%; Score 26; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPRV 5
11111
DB 1 GPRV 5

Search completed: June 27, 2003, 17:34:50
Job time : 27 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 17:42:03 ; Search time 39 Seconds
(without alignments)
22.185 Million cell updates/sec

Title: US-10-019-439-2

Perfect score: 51

Sequence: 1 GHRPLDKKR 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 3433

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	51.0	9	2	S39437 D-amino-acid oxida
2	25	49.0	11	2	JQ0395 hypothetical prote
3	23	45.1	18	2	I52614 u-plasminogen acti
4	22	43.1	17	2	A59069 excretory gland al
5	22	43.1	19	2	A37968 neural surface pro
6	21	41.2	12	2	S29859 gene p10 protein -
7	21	41.2	12	2	C34135 DNA-binding protei
8	21	41.2	17	4	I51887 hypothetical EMSRI
9	21	41.2	18	1	MTDFEC melanotropin beta
10	21	41.2	18	2	A55648 collagen alpha 1(X
11	21	41.2	18	2	S58855 botulinum neurotox
12	20	39.2	9	2	D58503 translation elonga
13	20	39.2	13	2	A23684 myosin heavy chain
14	20	39.2	13	2	B47415 mannose-1-phosphat
15	20	39.2	15	2	PU0143 carbon-monoxide de
16	20	39.2	16	2	S59901 pyruvate dehydroge
17	19	37.3	6	2	B56979 collagen alpha 1(I
18	19	37.3	9	2	PT0247 IG heavy chain CRD
19	19	37.3	12	2	C30503 collagen alpha 1(I
20	19	37.3	15	2	C56978 collagen alpha 1(I
21	19	37.3	16	2	H56978 collagen alpha 1(X
22	19	37.3	17	2	A47393 neuroleptide cala
23	19	37.3	17	2	I65274 glutathione S-tran
24	19	37.3	17	2	S78421 ribosomal protein
25	19	37.3	17	2	B48943 phase antigenic de
26	19	37.3	18	2	B32473 histidine-rich pro
27	19	37.3	19	2	S62864 toxin VI - Tityus
28	18	35.3	8	2	I64832 Ca2+-transporting
29	18	35.3	11	2	S45698 gamma-MSH-like pro

30	18	35.3	12	2	PN0046 ATP synthase D.cha
31	18	35.3	13	2	E39778 lactose phosphotra
32	18	35.3	13	2	I84603 deoxynucleotidyltr
33	18	35.3	15	2	PS0212 29K protein 4228 -
34	18	35.3	16	2	G45681 orf 61.1 - phage T
35	18	35.3	17	2	A34835 ribosomal protein
36	18	35.3	17	2	I49593 cystic fibrosis tr
37	18	35.3	17	2	I84733 gene CFTR protein
38	18	35.3	17	2	PH1802 T cell receptor al
39	18	35.3	17	2	PH1822 T cell receptor al
40	18	35.3	18	2	F27480 hydroxylase (EC 1.
41	18	35.3	19	2	S29766 cytochrome c (BDH)
42	18	35.3	19	2	A34467 36K microfibril-as
43	17	33.3	9	4	I57650 hemoglobin alpha c
44	17	33.3	10	2	A42089 transcription fact
45	17	33.3	11	2	A38841 rhodopsin homolog

ALIGNMENTS

RESULT 1
S39437
D-amino-acid oxidase (EC 1.4.3.3) - Trigonopsis variabilis (fragment)
C/Species: Trigonopsis variabilis
C/Date: 19-Mar-1997 #sequence_revision 05-Dec-1997 #text_change 07-May-1999
C/Accession: S39437
R/Schneider, T.; Andreassen, J.R.
Eur. J. Biochem. 218, 735-744, 1993
A/Title: Evidence for the functional importance of Cys298 in D-amino acid oxidase from
A/Reference number: S39437, PMID:94094869; PMID:7903639
A/Accession: S39437
A/Molecule type: protein
A/Residues: 1-9 <SCH>
A/Experimental source: CBS 4095
A/Function:
A/Description: oxidoreductase; catalyzes the oxidation of D-amino acids to their corres
A/Note: reoxidation of the enzyme by molecular oxygen is accompanied by the release of
C/Keywords: FAD; oxidoreductase

Query Match 51.0%; Score 26; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRP 4
DB 3 GHRP 6

RESULT 2

JQ0395
hypothetical protein (nodB 3' region) - Azorhizobium caulinodans
N/Alternate names: hypothethical 1.4K protein
C/Species: Azorhizobium caulinodans
A/Note: host Sesbania rostrata
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 03-Feb-1994
R/Accession: JQ0395
R/Goethals, K.; Gao, M.; Tomekpe, K.; Van Montagu, M.; Holsters, M.
Mol. Gen. Genet. 219, 289-298, 1989
A/Title: Common nodABC genes in Nod locus 1 of Azorhizobium caulinodans: nucleotide seq
A/Reference number: JQ0393; PMID:90136519; PMID:2615763
A/Accession: JQ0395
A/Molecule type: DNA
A/Residues: 1-11 <GOB>
A/Cross-references: GB:U18897
A/Experimental source: strain ORS571

Query Match 49.0%; Score 25; DB 2; Length 11;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 RPLDKKR 9
|:|||||

Db 2 RRDKR 8

RESULT 3

152614
u-plasminogen activator receptor precursor - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000
C/Accession: 152614
R/Soravita, E.; Grebe, A.; De Luca, P.; Hejin, K.; Suh, T.T.; Degen, J.L.; Blasl, F.
Blood 86, 624-635, 1995
A/Title: A conserved TATA-less proximal promoter drives basal transcription from the urc
A/Reference number: 152614; PMID:95329719; PMID:7605992
A/Accession: 152614
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-18 <RES>
A/Cross-references: GB:S78532; NID:G999307; PIDN:AD14289.1; PID:G4261989
C/Genetics:
A/Gene: UPAR
C/Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology

Query Match 45.1%; Score 23; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GHRPL 5
|||
Db 2 GHPPL 6

RESULT 4

A59069
excretory gland allergen Ansl - nematode (Anisakis simplex) (fragment)
C/Species: Anisakis simplex
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C/Accession: A59069
R/Moneo, I.
submitted to the Protein Sequence Database, September 1999
A/Reference number: A59069
A/Accession: A59069
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-17 <MON>
A/Experimental source: strain L3

Query Match 43.1%; Score 22; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 PLDK 7
|||
Db 8 PLDK 11

RESULT 5

A37968
neural surface protein Bravo - chicken (fragment)
C/Species: Gallus gallus (chicken)
C/Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 15-Aug-1997
C/Accession: A37968; A36345
R/de la Rosa, E.J.; Kayem, J.F.; Roman, J.M.; Stierhof, Y.D.; Dreyer, W.J.; Schwarz, U.
J. Cell Biol. 112, 1049, 1991
A/Reference number: A37968; PMID:91154309; PMID:1999455
A/Contents: extratum
A/Accession: A37968
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-19
R/de la Rosa, E.J.; Kayem, J.F.; Roman, J.M.; Stierhof, Y.D.; Dreyer, W.J.; Schwarz, U.
J. Cell Biol. 111, 3087-3096, 1990
A/Title: Topologically restricted appearance in the developing chick retinotectal system
A/Reference number: A36345; PMID:91100421; PMID:2269667

A/Accession: A36345
A/Molecule type: protein
A/Residues: 1-7,9-19

Query Match 43.1%; Score 22; DB 2; Length 19;
Best Local Similarity 80.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 PLDK 8
|||
Db 4 PLDK 8

RESULT 6

S29859
gene p10 protein - Choristoneura fumiferana nuclear polyhedrosis virus (fragment)
C/Species: Choristoneura fumiferana nuclear polyhedrosis virus, CFNPV
C/Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C/Accession: S29859
R/Hill, J.E.; Kuzio, J.; Wilson, J.A.; Mackinnon, E.A.; Faulkner, P.
Biochim. Biophys. Acta 1172, 187-189, 1993
A/Title: Nucleotide sequence of the p74 gene of a baculovirus pathogenic to the spruce
A/Reference number: S29849; PMID:93176808; PMID:8439559
A/Accession: S29859
A/Status: not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 1-12 <HL>
A/Experimental source: strain Ireland

Query Match 41.2%; Score 21; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 PLDKR 9
|||
Db 4 PLDKR 9

RESULT 7

C34135
DNA-binding protein s - Crithidia fasciculata mitochondrion (fragment)
C/Species: mitochondrion Crithidia fasciculata
C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 07-Dec-1999
C/Accession: C34135
R/Tittawella, I.
FEBS Lett. 260, 57-61, 1990
A/Title: Kinetoplast DNA-segregating proteins from the parasitic protozoan Crithidia fa
A/Reference number: A34135
A/Accession: C34135
A/Molecule type: protein
A/Residues: 1-12 <TT>
C/Genetics:
A/Genome: mitochondrion
A/Genetic code: SGC6
C/Keywords: mitochondrion

Query Match 41.2%; Score 21; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 GHRPLDK 8
|||
Db 3 GHSADAK 10

RESULT 8

I51887
hypothetical EMSR1/FLI1 mutant fusion protein, type 1 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000
C/Accession: I51887
R/Downing, J.R.; Head, D.R.; Parham, D.M.; Douglaes, E.C.; Hulsehof, M.G.; Link, M.P.; M
Am. J. Pathol. 143, 1294-1300, 1993

A;Title: Detection of the (11,22) (q24,q12) translocation of Ewing's sarcoma and peripheral
A;Reference number: 151887; MUID:94056652; PMID:8238248
A;Accession: 151887
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-17 <DOM>
A;Cross-references: GB:S66911; NID:g440935; PIDN:AAB28655.1; PID:g440936
C;Comment: This sequence is the chimeric product of a translocation mutation.
C;Genetics:
A;Gene: EMSR1/FLI1; EMS/FLI-1
A;Map position: 22q12.1/q24
C;Keywords: fusion protein

Query Match 41.2%; Score 21; DB 4; Length 17;
Best Local Similarity 60.0%; Pred. No. 1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 RPLDK 7
|||:
Db 4 RPDME 8

RESULT 9

MTDFBC
melanotropin beta - smaller spotted catshark
C;Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 23-Aug-1996
C;Accession: A01470
R;Love, R.M.; Pickering, B.T.
Gen. Comp. Endocrinol. 24, 398-404, 1974
A;Title: A beta-MSH in the pituitary gland of the spotted dogfish (Scyliorhinus canicula)
A;Reference number: A01470; MUID:75113445; PMID:4452470
A;Accession: A01470
A;Molecule type: protein
A;Residues: 1-18 <LOV>
C;Superfamily: corticotropin-1ipotropin
C;Keywords: hormone

Query Match 41.2%; Score 21; DB 1; Length 18;
Best Local Similarity 45.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 4; Gaps 1;

OY 1 GH----RPLDK 7
|||:
Db 8 GHFRGAPMDK 18

RESULT 10

A55648
collagen alpha 1(XI) chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 17-Mar-1999
C;Accession: A55648
R;Li, Y.; Lacerda, D.A.; Warman, M.L.; Beier, D.R.; Yoshioaka, H.; Ninomiya, Y.; Oxford,
J.; Taylor, B.A.; Seegmiller, R.E.; Olsen, B.R.
Cell 80, 423-430, 1995
A;Title: A fibrillar collagen gene, Col1a1, is essential for skeletal morphogenesis.
A;Reference number: A55648; MUID:55165095; PMID:7859283
A;Accession: A55648
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-18 <LIR>
C;Superfamily: collagen alpha 1(V) chain; fibrillar collagen carboxyl-terminal homology

Query Match 41.2%; Score 21; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 RPLDK 7
|||:
Db 7 KPLDR 11

RESULT 11
S58855
botulinum neurotoxin type B nontoxic-nonhemagglutinin component - Clostridium botulinum
N;Alternate names: NTN protein
C;Species: Clostridium botulinum
A;Variety: strain Eklund 17B
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 15-Oct-1999
C;Accession: S58855
R;East, A.K.; Stacey, J.M.; Collins, M.D.
Syst. Appl. Microbiol. 17, 306-312, 1994
A;Title: Cloning and sequencing of a hemagglutinin component of the botulinum neurotoxi
A;Reference number: S58855
A;Accession: S58855
A;Molecule type: DNA
A;Residues: 1-18 <EAS>
A;Cross-references: EMBL:X79103; NID:9870932; PIDN:CA55712.1; PID:9870933
A;Experimental source: strain Eklund 17B
C;Keywords: neurotoxin

Query Match 41.2%; Score 21; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 PLDKR 9
|||:
Db 12 PYDNKK 17

RESULT 12

D58503
translational elongation factor EF-Tu - unidentified bacterium (fragment)
C;Species: unidentified bacterium
C;Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 28-May-1999
C;Accession: D58503
R;Binette, J.P.; Binette, M.B.
Submitted to the Protein Sequence Database, October 1996
A;Description: The proteins of kidney and gallbladder stones.
A;Reference number: A58501
A;Accession: D58503
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <BIN>
A;Experimental source: human bile and stones
C;Superfamily: translation elongation factor Tu; translation elongation factor Tu homol
C;Keywords: GTP binding

Query Match 39.2%; Score 20; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHRP 4
|||:
Db 1 GYRP 4

RESULT 13

A23694
myosin heavy chain, smooth muscle - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 07-Feb-1997
C;Accession: A23694
R;Cole, D.G.; Yount, R.G.
J. Biol. Chem. 265, 22537-22546, 1990
A;Title: Photolabeling of the 6 and 10 S conformations of gizzard myosin with 3'-(2')-O-
A;Reference number: A23694; MUID:91093105; PMID:2266144
A;Accession: A23694
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-13 <COL>
C;Keywords: smooth muscle

Query Match 39.2%; Score 20; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 1.2e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPL 5
|||
:

Db 3 GHVPI 7

RESULT 14

B47415

mannose-1-phosphate guanylyltransferase (EC 2.7.7.13) 43K alpha chain - pig (fragment)

M:Alternate names: GDP-mannose pyrophosphorylase 43K alpha chain

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 25-Feb-1994 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996

C:Accession: B47415

R:Szmulo, T.; Drake, R.R.; York, J.L.; Elbein, A.D.

J. Biol. Chem. 268, 17943-17950, 1993

A:Title: GDP-mannose pyrophosphorylase. Purification to homogeneity, properties, and uti

A:Reference number: A47415; MUID:93352609; PMID:7688733

A:Accession: B47415

A:Molecule type: protein

A:Residues: 1-13 <SZU>

A:Experimental source: liver

C:Complex: The enzyme appears to be a heterodimer of alpha and beta chains.

C:Function:

A:Description: generates GDP-mannose and pyrophosphate from mannose-1-phosphate and GTP

A>Note: also catalyzes synthesis of GDP-glucose from glucose-1-phosphate (EC 2.7.7.34 ac

C:Keywords: blocked amino end; nucleotidyltransferase

Query Match

Best Local Similarity 39.2%; Score 20; DB 2; Length 13;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRP 4
|||

Db 6 HRP 8

RESULT 15

PL0143

carbon-monoxide dehydrogenase (EC 1.2.99.2) medium chain - Pseudomonas carboxydohydrogen

C:Species: Pseudomonas carboxydohydrogena

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993

C:Accession: PL0143

R:Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.

Arch. Microbiol. 152, 335-341, 1989

A:Title: Homology and distribution of CO dehydrogenase structural genes in carboxydotrop

A:Reference number: PL0138; MUID:90055678; PMID:2818128

A:Accession: PL0143

A:Molecule type: protein

A:Residues: 1-15 <KRA>

C:Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, me

C:Keywords: oxidoreductase

Query Match

Best Local Similarity 39.2%; Score 20; DB 2; Length 15;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRP 4
|||

Db 10 HRP 12

Search completed: June 27, 2003, 17:46:43
Job time : 40 secs

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OM protein - protein search, using sw model

Run on: June 27, 2003, 17:34:58 ; Search time 23 Seconds
(without alignments)
16.230 Million cell updates/sec

Title: US-10-019-439-2
Perfect score: 51
Sequence: 1 GHRPLDKR 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 1015

Minimum DB seq length: 0
Maximum DB seq length: 19

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	27	52.9	12 1 RS19_TOBBP	Q56251 tomato big
2	26	51.0	12 1 RS19_CLYEP	Q46490 clover yell
3	25	49.0	14 1 RS19_PRUPP	Q4160 prunus arme
4	24	47.1	12 1 RS19_ELYEP	Q47881 elm yellow
5	24	47.1	14 1 RS19_CLOBP	Q46228 clover prol
6	24	47.1	14 1 RS19_LOBPP	Q48878 loofah wic
7	22	43.1	15 1 UCL17_MAIZE	P80623 zea mays (m
8	21	41.2	18 1 MIB_SCYCA	P01206 scyllorhinu
9	20	39.2	9 1 PAR9_ASCSU	P43172 ascaris suu
10	20	39.2	15 1 DCMN_PSECH	P19917 pseudomonas
11	20	39.2	17 1 APID_BOMPA	P14646 bombus pasc
12	19	37.3	16 1 ALL1_CALVO	P41839 calliphora
13	19	37.3	19 1 SCX6_TITBA	P56610 titulus bahi
14	18.5	36.3	19 1 RS19_SPICI	O31159 spitioplasma
15	18	35.3	11 1 MUG_THETS	P41989 thermozon
16	18	35.3	11 1 UN05_CLOPA	P43350 clostridium
17	18	35.3	14 1 RS19_PMBPP	Q52093 pigeon pea
18	17	33.3	15 1 CYSK_CLOPA	P81344 clostridium
19	17	33.3	16 1 PPAC_BACME	P35948 bacillus me
20	16	31.4	3 1 GRWM_HUMAN	P01157 homo sapien
21	16	31.4	12 1 PPK4_PERAM	P82619 periplaneta
22	16	31.4	14 1 MCRX_METTM	P58815 methanobact
23	16	31.4	15 1 GR78_HORSE	P16397 equus cabal
24	16	31.4	15 1 UC23_MAIZE	P80629 zea mays (m
25	16	31.4	19 1 BRKM_BOMX	P83055 bombina max
26	16	31.4	19 1 PYRM_PSEFL	P56585 pseudomonas
27	15	29.4	10 1 TNKC_RANCA	P22690 rana catesb
28	15	29.4	13 1 NP4_LYMST	P80181 lymanaea sta
29	15	29.4	13 1 NP5_LYMST	P80182 lymanaea sta
30	15	29.4	13 1 RROC_MYCGA	P47716 mycoplasma
31	15	29.4	13 1 U15_HORVU	P34938 hordeum vul
32	15	29.4	16 1 LPHI_ECOLI	P03058 escherichia
33	15	29.4	16 1 TRYP_FELCA	P81071 felis silve

34	15	29.4	19 1 DHAB_COMTE	P80704 comamonas t
35	15	29.4	19 1 LPGE_ECOLI	P33236 escherichia
36	14	27.5	4 1 DCMN_PSECH	P19916 pseudomonas
37	14	27.5	7 1 UFE04_MOUSE	P38642 mus musculu
38	14	27.5	9 1 LITO_LITRAU	P08945 littoria aur
39	14	27.5	9 1 LITR_PHTRO	P08946 phyllomedus
40	14	27.5	9 1 NSK1_SARBU	P41492 sarcophaga
41	14	27.5	10 1 BRK_ONCMY	Q9P121 oncorhynch
42	14	27.5	10 1 GLEM_HUMAN	P02728 homo sapien
43	14	27.5	10 1 GON2_CHEPR	P80678 chelyosoma
44	14	27.5	10 1 GRP_RANRI	P23260 rana ridibu
45	14	27.5	10 1 LSK2_LEOMA	P09039 leucophaea

ALIGNMENTS

RESULT 1	RS19_TOBBP	STANDARD;	PRT;	12 AA.
ID	RS19_TOBBP			
AC	Q56251;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	30S ribosomal protein S19 (Fragment).			
GN	RPS5 OR RPS19.			
OS	Tomato big bud phytoplasma.			
OC	Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;			
OC	Acholeplasmataceae; Phycoplasma.			
OX	NCBI_TaxID=35770;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94350802; Pubmed=8071198;			
RA	Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;			
RT	"Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for			
RT	their classification."			
RL	J. Bacteriol. 176:5244-5254(1994).			
CC	-1- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY			
CC	TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.			
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CC	-----			
DR	EMBL; L27004; AAA83952.1; -			
DR	InterPro; IPR002222; Ribosomal S19.			
DR	PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.			
KW	Ribosomal protein; rRNA-binding.			
FT	NON TER 1			
SQ	SEQUENCE 12 AA; 1470 MW; 4CC88BBE90833AA3 CRC64;			
Query Match 52.9%; Score 27; DB 1; Length 12;				
Best Local Similarity 62.5%; Pred. No. 13;				
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
Qy	1 GHRPLDKK 8			
Db	1 GHMKDKK 8			
RESULT 2				
ID	RS19_CLYEP	STANDARD;	PRT;	12 AA.
AC	Q46490;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	30S ribosomal protein S19 (Fragment).			

```

GN RPS5 OR RPS19.
OS Clover yellow edge phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Phytoplasma.
OX NCBI_TaxID=35775;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94350802; PubMed=8071198;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
RT their classification.";
RL J. Bacteriol. 176:5244-5254(1994).
CC -1- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
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CC -----
DR EMBL; L27019; AAA83940.1; -
DR InterPro; IPR002222; Ribosomal S19.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER
SQ SEQUENCE 12 AA; 1409 MW; 4CC478EFC8333AA3 CRC64;

Query Match
Best Local Similarity 51.0%; Score 26; DB 1; Length 12;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GHRPLDKK 8
DB 1 GHAKDKK 8

RESULT 3
RS19_PRUP STANDARD; PRT; 14 AA.
AC 044160;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPS5 OR RPS19.
OS Prunus armeniaca phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Phytoplasma.
OX NCBI_TaxID=36589;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94350802; PubMed=8071198;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
RT their classification.";
RL J. Bacteriol. 176:5244-5254(1994).
CC -1- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
DR EMBL; L26994; AAA83934.1; -

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```

DR InterPro; IPR002222; Ribosomal S19.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER
SQ SEQUENCE 14 AA; 1756 MW; 4CC029E8FFFEA43 CRC64;

Query Match
Best Local Similarity 49.0%; Score 25; DB 1; Length 14;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GHRPLDKK 8
DB 3 GHAKDKK 10

RESULT 4
RS19_ELYEP STANDARD; PRT; 12 AA.
AC 047881;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPS5 OR RPS19.
OS Elm yellows phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Phytoplasma.
OX NCBI_TaxID=35774;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94350802; PubMed=8071198;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
RT their classification.";
RL J. Bacteriol. 176:5244-5254(1994).
CC -1- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
DR EMBL; L27022; AAA83942.1; -
DR InterPro; IPR002222; Ribosomal S19.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER
SQ SEQUENCE 12 AA; 1283 MW; 20C47B9D58333AA8 CRC64;

Query Match
Best Local Similarity 47.1%; Score 24; DB 1; Length 12;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 GHRPLDKK 8
DB 1 GHAKDKK 8

RESULT 5
RS19_CLOPP STANDARD; PRT; 14 AA.
AC 046228;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPS5 OR RPS19.
OS Clover proliferation phytoplasma.

```

OC Bacteria; Firmicutes; Mollicutes; Acholaeplasmatales;
 OC Acholaeplasmataceae; Phytolasma.
 OX NCBI_Taxid=35776;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94350802; Pubmed=8071198;
 RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
 RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
 their classification."
 RL J. Bacteriol. 176:5244-5254(1994).
 CC -1- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
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 CC -----
 DR EMBL: L27011; AAA83938.1; -
 DR InterPro: IPR002222; Ribosomal_S19.
 DR PROSITE: PS00323; RIBOSOMAL_S19; PARTIAL.
 KM Ribosomal protein; rRNA-binding.
 FT NON TER 1
 SQ SEQUENCE 14 AA; 1642 MW; 20C478B9FFFE4A8 CRC64;
 Query Match 47.1%; Score 24; DB 1; Length 14;
 Best Local Similarity 62.5%; Pred. No. 63;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GHRPLDKK 8
 DB 3 GHAKDKK 10
 Db 3 GHAKDKK 10
 RESULT 6
 RS19 LOWBP STANDARD; PRT; 14 AA.
 AC Q48878;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 30S ribosomal protein S19 (Fragment).
 GN RPS8 OR RPS19.
 OS Loofah witches'-broom phytolasma.
 OC Bacteria; Firmicutes; Mollicutes; Acholaeplasmatales;
 OC Acholaeplasmataceae; Phytolasma.
 OX NCBI_Taxid=35773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94350802; Pubmed=8071198;
 RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
 RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
 their classification."
 RL J. Bacteriol. 176:5244-5254(1994).
 CC -1- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
 TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE S19 FAMILY OF RIBOSOMAL PROTEINS.
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 CC -----
 DR EMBL: L27027; AAA83944.1; -
 DR InterPro: IPR002222; Ribosomal_S19.
 DR PROSITE: PS00323; RIBOSOMAL_S19; PARTIAL.

KM Ribosomal protein; rRNA-binding.
 FT NON TER 1
 SQ SEQUENCE 14 AA; 1642 MW; 20C478B9FFFE4A8 CRC64;
 Query Match 47.1%; Score 24; DB 1; Length 14;
 Best Local Similarity 62.5%; Pred. No. 63;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GHRPLDKK 8
 DB 3 GHAKDKK 10
 Db 3 GHAKDKK 10
 RESULT 7
 UC17 MAIZE STANDARD; PRT; 15 AA.
 AC P80623;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Unknown protein from 2D-page of etiolated coleoptile (Spot 32)
 (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Panicoideae; Andropogoneae; Zea.
 OX NCBI_Taxid=4577;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Coleoptile;
 RA Touzel P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Penoulet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 genome analysis program."
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.5, ITS MW IS: 42.7 kDa.
 CC Maize-2DPAGE; P80623; COLEOPTILE.
 DR MaizeDB; 123949; -
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 15 AA; 1554 MW; 0CAF15FFCECE8 CRC64;
 Query Match 43.1%; Score 22; DB 1; Length 15;
 Best Local Similarity 80.0%; Pred. No. 17e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 PLDKK 8
 DB 11 PLNKK 15
 Db 11 PLNKK 15
 RESULT 8
 MLB SCYCA STANDARD; PRT; 18 AA.
 ID ID SCYCA
 AC P01206;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Melanotropin beta (Beta-MSH).
 OS Scylliorhinus canicula (Spotted dogfish) (Spotted catshark).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphi; Galeoideae; Carcharhiniformes;
 OC Scylliorhinidae; Scylliorhinus.
 OX NCBI_Taxid=7830;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=7513445; Pubmed=4452470;
 RA Love R.M., Pickering B.T.;
 RT "A beta-MSH in the pituitary gland of the spotted dogfish
 (Scylliorhinus canicula): isolation and structure."
 RL Gen. Comp. Endocrinol. 24:398-404(1974).
 CC -1- SIMILARITY: BELONGS TO THE POMC FAMILY.

DR PIR; A01470; MTFBEC.
 KW Hormone.
 SQ SEQUENCE 18 AA; 2195 MW; 353C93A30C314DF4 CRC64;
 Query Match 41.2%; Score 21; DB 1; Length 18;
 Best Local Similarity 45.5%; Pred. No. 3.3e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 4; Gaps 1;

OY 1 GH----RPLD 7
 |||||
 8 GHFRWGAPEMDK 18

RESULT 9
 PAR9_ASCSU
 ID PAR9_ASCSU STANDARD; PRT; 9 AA.
 AC P43172;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE FMRPamide-like neuropeptide Ap9.
 OS Ascaris suum (pig roundworm) (Ascaris lumbricoides).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
 OC Ascarididae; Ascaris.
 OX NCBI_TaxID=6253;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95380362; PubMed=7651904;
 RA Cowden C., Stretton A.O.W.,
 RT "Eight novel FMRPamide-like neuropeptides isolated from the nematode
 RL Peptides 16:491-500(1995).
 CC -1- SIMILARITY: BELONGS TO THE PAR9 (FMRPAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES
 SQ SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;

Query Match 39.2%; Score 20; DB 1; Length 9;
 Best Local Similarity 80.0%; Pred. No. 1.1e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GHRPL 5
 |||||
 3 GPRPL 7

Db 3 GPRPL 7

RESULT 10
 DCMW_PSECH
 ID DCMW_PSECH STANDARD; PRT; 15 AA.
 AC P19917;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Carbon monoxide dehydrogenase medium chain (EC 1.2.99.2) (CO
 dehydrogenase subunit M) (CO-DH M) (Fragment).
 GN CUMT.
 OS Pseudomonas carboxydohydrogena.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Bradyrhizobium group.
 OX NCBI_TaxID=290;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90055678; PubMed=2818128;
 RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
 RT "Homology and distribution of CO dehydrogenase structural genes in
 RL Archaeobacterial bacteria.";
 RL Arch. Microbiol. 152:335-341(1989).
 CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
 dioxide.
 CC -1- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
 CC acceptor.
 CC -1- COFACTOR: FAD.

CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
 CC SMALL.
 DR PIR; P10143; P10143.
 KW Oxidoreductase; Flavoprotein; FAD.
 FT NON TER
 SQ SEQUENCE 15 AA; 1815 MW; 90508CF93E739D63 CRC64;
 Query Match 39.2%; Score 20; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 HRP 4
 |||||
 10 HRP 12

Db 10 HRP 12

RESULT 11
 APID_BOMPA
 ID APID_BOMPA STANDARD; PRT; 17 AA.
 AC P81464;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Apidaecin.
 OS Bombus pascuorum.
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
 OC Aculeata; Apoidea; Apidae; Bombus.
 OX NCBI_TaxID=65598;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Hemolymph;
 RX MEDLINE=97362903; PubMed=9219367;
 RA Rees U.A., Montatte M., Bulet P.;
 RT "Novel antibacterial peptides isolated from a European bumblebee,
 RL Bombus pascuorum (Hymenoptera, Apoidea)."
 RL Insect Biochem. Mol. Biol. 27:413-422(1997).
 CC -1- FUNCTION: ANTIBACTERIAL PEPTIDE ACTIVE AGAINST GRAM-NEGATIVE
 CC BACTERIA.
 CC -1- INDUCTION: BY BACTERIAL INFECTION.
 CC InterPro; IPR004828; Apidaecin.1.
 DR Pfam; PF00807; Apidaecin.1.
 KW Insect immunity; Antibiotic; Hemolymph.
 SQ SEQUENCE 17 AA; 1963 MW; CD1DD02C8BC23D1 CRC64;

Query Match 39.2%; Score 20; DB 1; Length 17;
 Best Local Similarity 60.0%; Pred. No. 5e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHRPL 5
 |||||
 1 GHRPV 5

Db 1 GHRPV 5

RESULT 12
 ALL1_CALVO
 ID ALL1_CALVO STANDARD; PRT; 16 AA.
 AC P41839;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Calliostatin 1 (leu-calliostatin 1) [Contains: Calliostatin 2 (leu-
 DE calliostatin 2) (leu-calliostatin 3) (leu-calliostatin 3)].
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Oestroidea; Calliphoridae; Calliphora.
 OX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Thoracic ganglion, Brain, and Head;
 RX MEDLINE=93211980; PubMed=8460157;
 RA Duve H., Johnsen A.H., Scott A.G., Yu C.G., Yagi K.J., Tobe S.S.,

RA Thorpe A.;
RT "Callistocactins: neuropeptides from the blowfly *Calliphora vomitoria*
RL with sequence homology to cockroach allatostatin.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
RN [2]
RP CHARACTERIZATION.
RA MEDLINE=94291167; PubMed=8020069;
RT Drove H., Thorpe A.;
RT "Distribution and functional significance of Leu-callatostatin in
the blowfly *Calliphora vomitoria*.";
RL Cell Tissue Res. 276:367-379(1994).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
A ROLE IN THE INTERACTION OF INFORMATION WITHIN THE BRAIN. MAY BE
INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO
CC FILLFIL A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
CC -1- TISSUE SPECIFICITY: BRAIN, SUBESOPHAGEAL GANGLION, RETROCRERERAL
CC COMPLEX, THORACICO-ABDOMINAL GANGLION, PERIPHERAL NEUROSECRETORY
CC SYSTEM AND INTESTINE.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
DR PIR: A47393; A47393.
DR PIR: B47393; B47393.
DR PIR: C47393; C47393.
KM Neuropeptide; Amidation.
FT PEPTIDE 1 16 CALIATOSTATIN 1.
FT PEPTIDE 3 16 CALIATOSTATIN 2.
FT PEPTIDE 9 16 CALIATOSTATIN 3.
FT MOD RES 16 16 AMIDATION.
SQ SEQUENCE 16 AA; 1907 MW; A435B68C26EC3D09 CRC64;

Query Match 37.3%; Score 19; DB 1; Length 16;
Best Local Similarity 50.0%; Pred. No. 7.4e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 PLODKR 9
Db 2 PLNEER 7

RESULT 13
SCX6_TITBA STANDARD; PRT; 19 AA.
ID SCX6_TITBA
AC P56610;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Toxin TbxX-VI (Fragment).
OS Tityus bahiensis (Brazilian scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butchoidea; Butidae; Tityus.
OX NCBI_Taxid=50343;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA MEDLINE=96190713; PubMed=8611151;
RA Beceril B., Corona M., Coronas F.I., Zamudio F.,
RA Calderon-Aranda E.S., Fletcher P.L. Jr., Martin B.M., Posani L.D.;
RT "Toxic peptides and genes encoding toxin gamma of the Brazilian
scorpions *Tityus bahiensis* and *Tityus stigmurus*.";
RL Biochem. J. 313:753-760(1996).
CC -1- FUNCTION: NOT TOXIC IN MICE.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
CC ALPHA-TOXIN SUBFAMILY.
DR InterPro: IPR002061; Scorpion_toxinL.
DR Pfam: PF00537; toxin_3.1.
FT NON TER 19
SQ SEQUENCE 19 AA; 2151 MW; 3535A2F1E5E67D14 CRC64;

Query Match 37.3%; Score 19; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 9e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 PLODKR 8
Db 6 PTDKR 10

RESULT 14
RS19_SPICI STANDARD; PRT; 19 AA.
ID RS19_SPICI
AC Q31159;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPS19.
OS Spiroplasma citri.
OC Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
OC Spiroplasmataceae; Spiroplasma.
OX NCBI_Taxid=2133;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 27556 / R9A2;
RA Le Dantec L., Sallard C., Bove J.M.;
RT "Nucleotide sequence of a part of the ribosomal proteins operon
S10-spc from *Spiroplasma citri*.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF031160; AAC35868.1;
DR InterPro: IPR002222; Ribosomal_S19.
DR Pfam: PF00203; Ribosomal_S19.1.
DR PROSITE: PS00323; RIBOSOMAL_S19; PARTIAL.
KM Ribosomal protein.
FT NON TER 1
SQ SEQUENCE 19 AA; 2190 MW; 517818B405DA70E9 CRC64;

Query Match 36.3%; Score 18.5; DB 1; Length 19;
Best Local Similarity 55.6%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 1 GHRPDKR 9
Db 10 GHGD-DKK 17

RESULT 15
MLG_THETS STANDARD; PRT; 11 AA.
ID MLG_THETS
AC P41989;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Melanotropin gamma (Gamma-melanocyte stimulating hormone) (Gamma-MSH).
OS Thermomyces tesulatum (leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;
OC Rhyndobellidae; Glossiphoniidae; Thermomyzom.
OX NCBI_Taxid=13286;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RA MEDLINE=94289944; PubMed=8026574;
RA Salzet M., Watez C., Bulet P., Malecha J.;
RT "Isolation and structural characterization of a novel peptide related
to gamma-melanocyte stimulating hormone from the brain of the leech

RT Theromyzon tessulatum."
RL FEBS Lett. 348:102-106(1994).
CC -1- SIMILARITY: BELONGS TO THE POMC FAMILY.
KW Hormone; Amidation.
PT MOD_RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1486 MW; 2DB8FAC6409C1E8 CRC64;

Query Match 35.3%; Score 18; DB 1; Length 11;
Best Local Similarity 57.1%; Pred. No. 7.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 4 GHRPMDK 10

Search completed: June 27, 2003, 17:44:34
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 17:40:08 ; Search time 76 seconds
(without alignments)
24.400 Million cell updates/sec

Title: US-10-019-439-2

Perfect score: 51

Sequence: 1 GHRPLDKR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 5270

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvivirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	51.0	14	2	Q46291
2	51.0	14	2	Q56750
3	51.0	16	8	Q9T206
4	49.0	19	11	Q9QXP9
5	47.1	19	10	Q94L06
6	45.1	18	4	Q9UM92
7	45.1	18	17	Q8ZTX6
8	45.1	19	8	Q63058
9	43.1	9	4	Q9UM87
10	43.1	10	2	Q8R3F1
11	43.1	15	2	P83331
12	43.1	19	5	Q8T8B6
13	41.2	12	13	Q9PSW5
14	41.2	14	15	Q98Y97
15	41.2	18	2	Q45866
16	41.2	19	12	Q83965

17	20	39.2	10	2	Q47561	Q47561 escherichia
18	20	39.2	11	11	Q62207	Q62207 mus musculus
19	20	39.2	15	2	Q8RKN0	Q8RKN0 escherichia
20	20	39.2	17	4	Q16231	Q16231 homo sapien
21	20	39.2	17	6	Q95W99	Q95W99 equus caball
22	20	39.2	17	12	Q85719	Q85719 reovirus (c
23	20	39.2	18	6	Q8SQ45	Q8SQ45 oryctolagus
24	19	37.3	9	11	Q08979	Q08979 mus musculus
25	19	37.3	12	11	Q54970	Q54970 mus musculus
26	19	37.3	13	4	Q9UCS4	Q9UCS4 homo sapien
27	19	37.3	15	4	Q9UGA5	Q9UGA5 homo sapien
28	19	37.3	15	8	P82135	P82135 spinacia ol
29	19	37.3	15	10	P82442	P82442 nicotiana t
30	19	37.3	16	11	Q9R2D2	Q9R2D2 mus musculus
31	19	37.3	16	12	P90290	P90290 barley mild
32	19	37.3	17	2	Q06946	Q06946 salmonella
33	19	37.3	18	8	Q8SKX0	Q8SKX0 cuscuta ref
34	19	37.3	18	9	Q92X80	Q92X80 lactococcus
35	19	37.3	19	4	Q9UH46	Q9UH46 homo sapien
36	19	37.3	19	4	Q8WV79	Q8WV79 homo sapien
37	19	37.3	19	4	Q9UC21	Q9UC21 homo sapien
38	19	37.3	19	12	Q90622	Q90622 simian hep
39	19	37.3	19	12	Q90628	Q90628 simian hep
40	19	37.3	19	16	Q935K9	Q935K9 salmonella
41	18.5	36.3	19	15	Q905F6	Q905F6 human immun
42	18	35.3	8	4	Q16468	Q16468 homo sapien
43	18	35.3	13	2	Q9R8R9	Q9R8R9 streptococ
44	18	35.3	13	4	Q14182	Q14182 homo sapien
45	18	35.3	14	4	Q8TD29	Q8TD29 homo sapien

ALIGNMENTS

RESULT 1

Q46291 PRELIMINARY; PRT; 14 AA.

AC Q46291; Q46291; (T-EMBLrel. 01, Created)

DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)

DT 01-NOV-1996 (T-EMBLrel. 19, Last annotation update)

DE Ribosomal protein S19 (Fragment).

OS Canadian peach X phytoplasma.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;

OC Acholeplasmatales; Acholeplasmataceae; Phytoplasma.

OX NCBI_TaxID=35778;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=94350802; PubMed=8071198;

RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;

RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for

RT their classification."

RL U. Bacteriol. 176:5244-5254(1994).

DR EMBL; L27016; AAA83950.1; -.

FT NON TER 1 1

SQ SEQUENCE 14 AA; 1712 MW; 4CC478BFF8FF54A3 CRC64;

Query Match 51.0%; Score 26; DB 2; Length 14;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHRPLDKK 8
Db 3 GHRPLDKK 10

RESULT 2

Q56750 PRELIMINARY; PRT; 14 AA.

DT 01-NOV-1996 (T-EMBLrel. 01, Created)

DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)

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DE Ribosomal protein S19 (Fragment).
OC Western X phytolasma.
OC Bacteria: Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Acholoplasmatales; Acholoplasmataceae; Phytolasma.
OX NCBI_TaxID=37704;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94350802; PubMed=8071198;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
RL their classification.";
DR EMBL; L27047; AAA83948.1; -.
FT NON_TER
SQ SEQUENCE 14 AA; 1712 MW; 4CC478E8FFFE4A3 CRC64;

Query Match
Best Local Similarity 51.0%; Score 26; DB 2; Length 14;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GHRPLDK 8
Db 3 GHAKDKX 10

RESULT 3
Q9T206 PRELIMINARY; PRT; 16 AA.
AC Q9T206;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE Cytochrome-C reductase 11 kDa subunit (EC 1.10.2.2) (Fragment).
OS Solanum tuberosum (Potato).
OC Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OX Asteridae; eusterids I; Solanales; Solanaceae; Solanum.
RN NCBI_TaxID=4113;
RP [1]
RP SEQUENCE.
RX MEDLINE=94198758; PubMed=7764624;
RA Braun H.P., Krutz V., Schmitz U.K.;
RL Planta 193:99-106(1994).
SQ SEQUENCE 16 AA; 1904 MW; AFC237AE7549E2B5 CRC64;

Query Match
Best Local Similarity 51.0%; Score 26; DB 8; Length 16;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 10 GORPYDE 16

RESULT 4
Q9QXP9 PRELIMINARY; PRT; 19 AA.
ID Q9QXP9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE Hepatocyte nuclear factor-3 beta (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J;
RA Maeyama K., Yoshihashi H., Kosaki R., Suzuki T., Kosaki K.;
"Mus musculus (C57BL/6J) HNF3-beta gene, promoter region.";
SQ

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RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF191558; AAF25196.1; -.
FT NON_TER
SQ SEQUENCE 19 AA; 2187 MW; 5AD23E9ADD1B5079 CRC64;

Query Match
Best Local Similarity 49.0%; Score 25; DB 11; Length 19;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLD 6
Db 9 GHRPSD 14

RESULT 5
Q94L06 PRELIMINARY; PRT; 19 AA.
ID Q94L06;
AC Q94L06;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE Isoopropyl malate synthase (Fragment).
GN MY24-1-BN-7.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OX eurosids II; Brassicales; Brassicaceae; Brassica.
RN NCBI_TaxID=3708;
RP [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CV_YUDAL;
RA Fournann M., Froger N., Brunel D.;
RT "Amplified consensus gene markers: Tools designing for a genetic map
RL of Arabidopsis-known-function genes in Brassica.";
DR EMBL; AF258256; AAK49052.1; -.
FT NON_TER
SQ SEQUENCE 19 AA; 1989 MW; A41FC1E46CFC0E6D CRC64;

Query Match
Best Local Similarity 47.1%; Score 24; DB 10; Length 19;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLDK 7
Db 2 GNAPLEK 8

RESULT 6
Q9UM92 PRELIMINARY; PRT; 18 AA.
ID Q9UM92;
AC Q9UM92;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE UPAR protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95329719; PubMed=7605992;
RA Soravia E., Grebe A., De Luca P., Helin K., Suh T.T., Degen J.L.,
RA Blasi F.;
RT "A conserved TATA-less proximal promoter drives basal transcription
RT from the uridine-type plasminogen activator receptor gene.";
RL Blood 86:624-635(1995).
DR EMBL; S78532; AAD14289.1; -.
FT NON_TER
SQ SEQUENCE 18 AA; 1964 MW; 617216DF83DE726C CRC64;

```

Query Match 45.1%; Score 23; DB 4; Length 18;
 Best Local Similarity 80.0%; Pred. No. 1e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GHRPL 5
 DB 2 GHRPL 6

RESULT 7

08ZTX6 PRELIMINARY; PRT; 18 AA.
 AC 08ZTX6;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Ribosomal protein l39E, frameshift.
 GN PA3044A.
 OS Pyrobaculum aerophilum.
 OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
 OC Thermoproteaceae; Pyrobaculum.
 OX NCBI_TaxID=13773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
 RX PubMed=11792869;
 RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
 RT Miller J.H.;
 RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
 aerophilum.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989 (2002).
 DR EMBL; AE009908; AL64633.1; -.
 KM Complete proteome.
 SQ SEQUENCE 18 AA; 2013 MW; ED5FEC28E49FCB6 CRC64;

Query Match 45.1%; Score 23; DB 17; Length 18;
 Best Local Similarity 57.1%; Pred. No. 1e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 HRPLDKK 8
 DB 4 NKPLGKK 10

RESULT 8

063058 PRELIMINARY; PRT; 19 AA;
 AC 063058;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Ribosomal protein S11 (Fragment).
 GN RBS11.
 OS Lathraea clandestina.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Lamiales; Orobanchaceae; Lathraea.
 OX NCBI_TaxID=41911;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lusson N., Delavault P., Thalaoun P.;
 RT "The rbcL gene from Lathraea (holoparasitic) is not transcribed by a
 plastid-encoded RNA polymerase.";
 RL Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF030983; AAC16521.1; -.
 DR InterPro; IPR001971; Ribosomal_S11.
 DR Pfam; PF00411; Ribosomal_S11; I.
 DR Chloroplast.
 FT NON TER 1 1
 SQ SEQUENCE 19 AA; 2245 MW; 130D2AB3FE680B24 CRC64;

Query Match 45.1%; Score 23; DB 8; Length 19;
 Best Local Similarity 55.6%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 GHRPLDKK 9
 DB 10 GCRPPKKR 18

RESULT 9

09UM87 PRELIMINARY; PRT; 9 AA.
 AC 09UM87;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE FGFR2 protein (Fragment).
 GN FGFR2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96253074; PubMed=8676562;
 RA Wada C., Ishigaki M., Toyo-oka Y., Yamabe H., Ohnuki Y., Takada F.,
 RA Yamazaki Y., Ohnuki H.;
 RT "Nucleotide sequences at intron 6 and exon 7 junction of fibroblast
 growth factor receptor 2 and rapid mutational analysis in Apert
 syndrome.";
 RT Rinsbo Byori 44:435-438 (1996).
 DR EMBL; S82438; AAD14392.1; -.
 FT NON TER 1 1
 SQ SEQUENCE 9 AA; 1103 MW; 9E4D20477401F775 CRC64;

Query Match 43.1%; Score 22; DB 4; Length 9;
 Best Local Similarity 75.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 HRPL 5
 DB 4 HRPI 7

RESULT 10

08RJF1 PRELIMINARY; PRT; 10 AA.
 AC 08RJF1;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Porin-like protein (Fragment).
 OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=294;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NC16-2, TC29-5, AND TC97;
 RC TRANSPOSON=TN5041A1, TN5041B, AND TN5041D1;
 RA Kholodil G.Y., Gorlenko Z.M., Mindlin S.Z., Nikiforov V.G.;
 RT "Distribution of distinct microvariants of TN5041 in environmental
 bacteria.";
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ422128; CAD19527.1; -.
 DR EMBL; AJ422129; CAD19528.1; -.
 DR EMBL; AJ422130; CAD19529.1; -.
 FT NON TER 10 10
 SQ SEQUENCE 10 AA; 1206 MW; 23C47E7401F5A17 CRC64;

Query Match 43.1%; Score 22; DB 2; Length 10;
 Best Local Similarity 75.0%; Pred. No. 9e+02;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 HRPLD 5
 |||:
 Db 6 HRPI 9

RESULT 11

PRELIMINARY; PRT; 15 AA.
 ID P83331
 AC P83331;
 DT 01-JUN-2002 (T-EMBLrel. 21, Created)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
 DE Penicillin-binding protein (BBP) (Fragment).
 OS Streptococcus thermophilus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 NCBI_TaxID=1308;
 RX STRAIN=ITG8T80;
 RA Guimont C., Chopard M.A., Galliard J.L., Chamba J.F.;
 RT "Comparative study of the protein composition of three strains of
 RT Streptococcus thermophilus grown either in M17 medium or in milk."
 RL Laite 0:0-0(2002).
 KW Peptidoglycan synthesis; Cell wall.
 FT NON_TER 1
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1653 MW; 19E60997E2C4D945 CRC64;

Query Match 43.1%; Score 22; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLD 6
 |||:
 Db 7 GYAPID 12

RESULT 12

PRELIMINARY; PRT; 19 AA.
 ID Q8T8B6
 AC Q8T8B6;
 DT 01-JUN-2002 (T-EMBLrel. 21, Created)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
 DE Choline acetyltransferase (Fragment).
 GN CI-CHAT.
 OS Clona intestinalis.
 OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 OC Phlebobranchia; Cloniidae; Clona.
 NCBI_TaxID=7719;
 RX MEDLINE=21863848; PubMed=11875658;
 RA Takamura K., Egawa T., Ohnishi S., Okada T., Fukuoaka T.;
 RT "Developmental expression of ascidian neurosecretory synthesis
 RT genes. Choline acetyltransferase and acetylcholine transporter
 RT genes.";
 RL Dev. Genes Evol. 212:50-53(2002).
 DR EMBL; AB072000; BAB85861.1; -.
 KW Transferase.
 FT NON_TER 19
 FT NON_TER 19
 SQ SEQUENCE 19 AA; 2176 MW; 36DC3BCDC6A922F CRC64;

Query Match 43.1%; Score 22; DB 5; Length 19;
 Best Local Similarity 50.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 RPLDKX 8
 |||:
 Db 8 KPLEKR 13

RESULT 13
 Q9PSW5
 AC Q9PSW5;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last annotation update)
 DE I kappa B-alpha (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RX MEDLINE=96125200; PubMed=8543172;
 RA Krishnan V.A., Schatzle J.D., Hinojos C.M., Bose H.R. Jr.;
 RT "Structure and regulation of the gene encoding avian inhibitor of
 RT nuclear factor kappa B-alpha."
 RL Gene 166:261-266(1995).
 DR EMBL; L27342; AAA92641.1; -.
 FT NON_TER 12
 FT NON_TER 12
 SQ SEQUENCE 12 AA; 1276 MW; E584F64824C77401 CRC64;

Query Match 41.2%; Score 21; DB 13; Length 12;
 Best Local Similarity 60.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HRPLD 6
 |||:
 Db 5 HRDAE 9

RESULT 14

PRELIMINARY; PRT; 14 AA.
 ID Q98Y97
 AC Q98Y97;
 DT 01-JUN-2001 (T-EMBLrel. 17, Created)
 DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (T-EMBLrel. 17, Last annotation update)
 DE Truncated pol protein (Fragment).
 GN POL.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11676;
 RX MEDLINE=996664;
 RA Schmidt B., Walter H., Moschik G., Patz C., Werwein M., Schwingel E.,
 RA Korn K.;
 RT "Recovery of HIV-1 pol gene sequences by direct sequencing of
 RT amplified products derived from plasma samples."
 RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF347572; AAK32648.1; -.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 14 AA; 1748 MW; C2921F7CAE276416 CRC64;

Query Match 41.2%; Score 21; DB 15; Length 14;
 Best Local Similarity 71.4%; Pred. No. 2e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 RPLDKR 9
 |||:
 Db 8 RPLVLR 14

RESULT 15

PRELIMINARY; PRT; 18 AA.
 ID Q45866
 AC Q45866;
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE NINH protein.
 GN NINH.
 OS Clostridium botulinum.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 CC Clostridiales; Clostridiaceae; Clostridium.
 OX NCBI_TaxID=1491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=17B;
 RA East A.K., Stacey J.M., Collins M.D.;
 RT "Cloning and sequencing of a hemagglutinin component of the botulinum
 neurotoxin complex encoded by Clostridium botulinum types A and B.";
 RL Syst. Appl. Microbiol. 17:306-312(1994).
 DR EMBL; X79103; CAAS5712.1; -.
 SO SEQUENCE 18 AA; 2029 MW; D4DD49856A10DFD9 CRC64;

Query Match 41.2%; Score 21; DB 2; Length 18;
 Best Local Similarity 50.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 PLDKKR 9
 | : | : | :
 Db 12 PVDNKK 17

Search completed: June 27, 2003, 17:45:58
 Job time : 78 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 27, 2003, 17:34:23 ; Search time 69 Seconds
(without alignments)
17.381 Million cell updates/sec

Title: US-10-019-439-2
Perfect score: 51
Sequence: 1 GHRPLDKKR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 278369

Minimum DB seq length: 0
Maximum DB seq length: 19

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	9	22	ABR76979
2	51	100.0	10	16	AAW11931
3	51	100.0	12	13	AAW28629
4	51	100.0	12	14	AAW44829
5	51	100.0	16	14	AAW44830
6	41	80.4	7	8	AAW71314
7	41	80.4	7	11	AAW05558
8	41	80.4	7	15	AAW53269
9	41	80.4	7	15	AAW5792
10	41	80.4	8	9	AAW82686

11	41	80.4	8	14	AAW44837	Human fibrin beta-Synthetic beta-pep
12	41	80.4	8	15	AAW63270	Fibrin-specific ep
13	41	80.4	8	15	AAW63270	Human fibrin beta-
14	41	80.4	12	14	AAW44838	Fibrinogen-beta pe
15	36	70.6	11	21	AAW10656	Fibrinogen-beta c
16	36	70.6	11	21	AAW10629	GST-FYN SH3 protei
17	30	58.8	12	16	AAW34400	Multiply branched
18	29	56.9	12	19	AAW65555	Multiply branched
19	27	52.9	11	19	AAW65554	Human peptide #277
20	27	52.9	14	22	AAW97002	Human BCL2 immunog
21	27	52.9	17	19	AAW20168	HEV ORF1 peptide
22	27	52.9	18	14	AAW44726	Accelerator peptid
23	26	51.0	4	16	AAW62426	Non-crosslinked pr
24	26	51.0	4	20	AAW31030	Synthetic fibrinog
25	26	51.0	5	18	AAW34571	Thrombin cleavage
26	26	51.0	5	21	AAW37079	Human platelet gly
27	26	51.0	10	18	AAW32704	Human microtubule
28	26	51.0	12	19	AAW20425	SV40 large T anti
29	26	51.0	13	21	AAW20990	TNF-antagonist pep
30	26	51.0	15	21	AAW17973	Fragment of human
31	26	51.0	15	21	AAW76276	Ubiquitin 9 conjug
32	26	51.0	15	22	AAW51531	Interferon-gamma s
33	26	51.0	15	22	AAW88149	Interferon-gamma s
34	26	51.0	15	22	AAW88150	Immunomodulating
35	26	51.0	15	22	AAW84079	TNF-alpha antagont
36	26	51.0	15	22	AAW84092	gp100 derived IFN-
37	26	51.0	15	22	AAW97759	gp100 derived IFN-
38	26	51.0	15	22	AAW97750	gp100 derived IFN-
39	26	51.0	15	23	AAW72935	Tumour necrosis fa
40	26	51.0	17	20	AAW02812	Fragment of human
41	26	51.0	17	22	AAW06674	Ping-3 peptide of
42	26	51.0	19	21	AAW76363	Fragment of human
43	25	49.0	9	16	AAW21473	Collagenase (fibro
44	25	49.0	9	20	AAW48833	Membrane dipeptida
45	25	49.0	9	23	AAW75028	Mo-MuLV variable r

ALIGNMENTS

RESULT 1
ABW76979 standard; peptide; 9 AA.

ID	ABW76979	standard; peptide; 9 AA.
XX	ABW76979;	
AC	22-JUL-2002 (first entry)	
XX	Residues 45-54 of human fibrinogen beta chain precursor.	
DE	Anti-arthritis; anti-inflammatory; fibrin; rheumatoid polyarthritis;	
KW	human; fibrinogen beta chain.	
XX	Homo sapiens.	
XX	FR295735-A1.	
PN	05-JAN-2001.	
XX	01-JUL-1999; 99FR-0008470.	
XX	01-JUL-1999; 99FR-0008470.	
XX	01-JUL-1999; 99FR-0008470.	
XX	(UYTO-) UNIV TOULOUSE SABATIER PAUL.	
XX	Setre G, Sebbag M;	
XX	WPI; 2001-114394/13.	
DR	New citrulline-containing polypeptide from fibrin, useful for diagnosis	
PT	and treatment of rheumatoid polyarthritis	
XX	Example 1; Page 12; 23pp; French.	

```

XX CC The present invention relates to a citrulline (Cit) containing
CC polypeptide derived from all or part of the alpha- or beta-chains of
CC fibrin by substitution of at least one arginine residue by Cit. The Cit
CC containing polypeptides can be used for in vitro diagnosis of rheumatoid
CC polyarthritis (RP), by detecting disease-specific autoantibodies, and
CC therapeutically for neutralising the RP-associated autoimmune response.
CC The present sequence is a fragment (residues 45-54) of the human
CC fibrinogen beta chain precursor, which was used in an example from the
CC invention.
XX
SQ Sequence 9 AA;

Query Match 100.0%; Score 51; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKR 9
Db 1 GHRPLDKR 9

RESULT 2
AAW11931
ID AAW11931 standard; peptide; 10 AA.
XX
AC AAW11931;
XX
DT 02-APR-1997 (first entry)
XX
DE Fibrinogen A-alpha-chain residues 17-26.
XX
KW Monoclonal; antibody; human; soluble; fibrin; fibrinogen;
KW urea-treated; des-AAB; A-alpha-chain; immunoassay; diagnosis;
KW disseminated intravascular coagulation.
XX
OS Homo sapiens.
XX
PN WO9512617-A1.
XX
PD 11-MAY-1995.
XX
PF 01-NOV-1994; 94WO-0P01844.
XX
PR 02-NOV-1993; 93JP-0297325.
XX
PA (IATR ) IATRON LAB INC.
XX
PI Imuzuka K, Ito Y, Kohno I, Soe G;
XX
DR WPI; 1995-206667/27.
XX
PT Monoclonal antibody reactive with soluble human fibrin - but not
PT with fibrinogen, is useful for fibrin immunoassay in plasma
PT specimens
XX
PS Example 3; Page 15; 32pp; Japanese.
XX
CC A novel monoclonal antibody (MAB) reacts with human soluble fibrin,
CC but not with human fibrinogen. Specifically when the MAB reacts
CC with urea-treated des-AAB fibrin the reaction is not inhibited by
CC peptides corresponding to fibrinogen A-alpha-chain residues 17-26
CC (AAW11931), B-beta-chain residues 15-24 (AAW11932) or gamma-chain
CC residues 312-324 (AAW11933). The MAB is useful in immunoassays for
CC soluble fibrin in plasma samples (e.g. by sandwich immunoassay),
CC particularly for the diagnosis of pathological conditions such as
CC disseminated intravascular coagulation.
XX
SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GHRPLDKR 9
Db 1 GHRPLDKR 9

RESULT 3
AAR28629
ID AAR28629 standard; peptide; 12 AA.
XX
AC AAR28629;
XX
DT 22-MAR-1993 (first entry)
XX
DE N-terminal human fibrin peptide.
XX
KW bispecific hybrid monoclonal antibody; thrombolytic agent;
KW cardiac infarction; arterial embolism; cerebral infarction;
KW peripheral arterial/venous obstruction; retinal arterial obstruction.
XX
OS Homo sapiens.
XX
PN EP513778-A.
XX
PD 19-NOV-1992.
XX
PE 14-MAY-1992; 92EP-0108134.
XX
PR 17-MAY-1991; 91JP-0112874.
XX
PR 13-MAR-1992; 92JP-0055025.
XX
PA (TAKE ) TAKEDA CHEM IND LTD.
XX
PI Iwasa S, Kurokawa T, Watanabe A;
XX
DR WPI; 1992-383677/47.
XX
PT Bi-specific antibody useful for treating thrombotic obstructive
PT diseases e.g. Cardiac infarction - comprises antithrombus
PT antibody variable region and anti-thrombolytic substance antibody
PT variable region with no heavy chain constant region domains 2 and
PT 3
XX
PS Disclosure; Page 3; 30pp; English.
XX
CC This sequence represents an N-terminal peptide of human fibrin. It
CC was used in the production of bispecific monoclonal antibodies which
CC are specific for fibrins, but do not bind fibrinogen, and are
CC specific for anti-thrombolytic substance. The compsn. contg. these
CC Abs lacks the side effects of prior art Ab targetted thrombolytic
CC agents and has enhanced thrombolytic activity.
XX
SQ Sequence 12 AA;

Query Match 100.0%; Score 51; DB 13; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLDKR 9
Db 1 GHRPLDKR 9

RESULT 4
AAR44829
ID AAR44829 standard; peptide; 12 AA.
XX
AC AAR44829;
XX
DT 20-JUN-1994 (first entry)
XX
DE Human fibrin beta-chain N-terminal peptide (1-11)-Cys.
XX

```

KM Tissue plasminogen activator; t-PA; murein; fibrin; antigen;
 KM anti-fibrin; monoclonal antibody; hybridoma; thrombolysis
 KM antithrombotic agent; bispecific antibody.
 XX
 OS Synthetic.
 FH Key
 FT Region
 FT 1..11
 FT /note= "human fibrin beta-chain residues 1-11"
 FT Modified-site
 FT 12
 FT /note= "BSA carrier is attached to Cys"
 PN JF05304992-A.
 XX
 PD 19-NOV-1993.
 PF 17-JUN-1992; 92JP-0158301.
 XX
 PR 20-JUN-1991; 91JP-0148936.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 DR WPI; 1993-408334/51.
 PT Hybrid monoclonal antibody - used for prepn. of thrombolytic drug
 PT having increased thrombolytic activity and specificity and
 PT reduced reactivity to fibrinogen
 XX
 PS Disclosure; Page 9; 38pp; Japanese.
 CC Human fibrin beta-chain N-terminal peptide (1-11)-Cys was
 CC synthesised and coupled to BSA for injection into mice. The peptide
 CC was used to raise antibodies to human fibrin. Monoclonal antibodies
 CC specific for fibrin are used in the production of bispecific
 CC monoclonal antibodies which also recognise truncated tPA muteins
 CC lacking the finger, EGF and Kringle 1 domains.
 CC
 XX
 SQ Sequence 12 AA;
 Query Match 100.0%; Score 51; DB 14; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.00071;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDKKR 9
 Db 1 GHRPLDKKR 9
 RESULT 5
 AAR44830
 ID AAR44830 standard; peptide; 16 AA.
 XX
 AC AAR44830;
 DT 20-JUN-1994 (first entry)
 XX
 DE Human fibrin beta-chain internal peptide fragment.
 XX
 KM Tissue plasminogen activator; t-PA; murein; fibrin; antigen;
 KM anti-fibrin; monoclonal antibody; hybridoma; thrombolysis
 KM antithrombotic agent; bispecific antibody.
 XX
 OS Synthetic.
 FH Key
 FT Region
 FT 1..11
 FT /note= "human fibrin beta-chain residues 1-11"
 FT Modified-site
 FT 12
 FT /note= "BSA carrier is attached to Cys"
 PN JF05304992-A.
 XX
 PD 19-NOV-1993.
 PF 17-JUN-1992; 92JP-0158301.
 XX
 PR 20-JUN-1991; 91JP-0148936.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.

XX
 DR WPI; 1993-408334/51.
 XX
 PT Hybrid monoclonal antibody - used for prepn. of thrombolytic drug
 PT having increased thrombolytic activity and specificity and
 PT reduced reactivity to fibrinogen
 XX
 PS Disclosure; Page 9; 38pp; Japanese.
 CC Human fibrin internal peptide fragment was identified as a
 CC candidate immunogen to raise antibodies to human fibrin. Monoclonal
 CC antibodies specific for fibrin are used in the production of bispecific
 CC monoclonal antibodies which also recognise truncated tPA muteins
 CC lacking the finger, EGF and Kringle 1 domains.
 CC
 XX
 SQ Sequence 16 AA;
 Query Match 100.0%; Score 51; DB 14; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.00098;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GHRPLDKKR 9
 Db 6 GHRPLDKKR 14
 RESULT 6
 AAP71314
 ID AAP71314 standard; peptide; 7 AA.
 XX
 AC AAP71314;
 DT 03-OCT-2002 (updated)
 DT 19-JUN-1991 (first entry)
 XX
 DE Sequence of fibrin immunogen for the prepn. of monoclonal antibodies
 DE (MAbs).
 XX
 KM Fibrin-specific monoclonal antibody; screening.
 XX
 OS Homo sapiens.
 FH Key
 FT Misc-difference 7
 FT Location/Qualifiers
 FT /label= Lys-OH
 XX
 PN W08706263-A.
 XX
 PD 22-OCT-1987.
 PF 14-APR-1987; 87WO-US00862.
 XX
 PR 14-APR-1986; 86US-0851514.
 XX
 PA (GENO-) GEN HOSPITAL CORP.
 PA (GENO-) GEN HOSPITAL CORP.
 XX
 PI Matsueda GR, Haber E;
 XX
 DR WPI; 1987-306855/43.
 XX
 PT Screening of fibrin-specific monoclonal antibodies - by contact
 PT with immobilised crosslinked fibrin clot and screening with
 PT detectable labelling step
 XX
 PS Disclosure; Page 7; 41pp; English.
 CC The MAbs are specific to fibrin without fibrinogen cross-reactivity.
 CC They have increased binding to in vitro and in vivo thrombi. The
 CC MAbs can be used in immunoassays for fibrin in the presence of
 CC fibrinogen or other proteins. They can be used as immunofluorescent
 CC ligands for the purification of fibrin.
 CC (Updated on 03-OCT-2002 to add missing OS field.)

XX
SQ Sequence 7 AA;

Query Match 80.4%; Score 41; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHRPLDK 7
1 GHRPLDK 7
DB 1 GHRPLDK 7

RESULT 7
AAR05558
ID AAR05558 standard; peptide; 7 AA.

AC AAR05558;

DT 11-OCT-1990 (first entry)

DE Peptide antigenic to fibrin.

KM fibrin; fibrinogen; thrombi; immunoaffinity.

OS Synthetic.

Key Location/Qualifiers

FT Misc-difference 2 /label=His or Pro

FT Misc-difference 4 /label=Pro or Val

FT Misc-difference 5 /label=Leu or Val

FT Misc-difference 6 /label=Asp or Glu

FT Misc-difference 7 /label=Lys or Arg

PN US4927916-A.

PD 22-MAY-1990.

PF 30-JAN-1986; 86US-0824228.

PR 23-APR-1984; 84US-0603155.

PR 30-JAN-1986; 86US-0824228.

PA (GEHO-) GEN HOSPITAL CORP.

PI Matsueda GR, Haber E, Hui K;

DR WPI; 1990-185723/24.

PT Fibrin-specific monoclonal antibodies -

PT lacking fibrinogen cross-reactivity, obd. using peptide(s)

PS Claim 1; Page 17; 12pp; English.

CC Peptide is epitopic to fibrin, allowing anti-fibrin Abs to be

CC raised without cross-reactivity to fibrinogen. They are

CC particularly useful in detection of fibrin and thrombi.

SQ Sequence 7 AA;

Query Match 80.4%; Score 41; DB 11; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHRPLDK 7
1 GHRPLDK 7
DB 1 GHRPLDK 7

RESULT 8
AAR63269
ID AAR63269 standard; peptide; 7 AA.

AC AAR63269;

DT 21-JUL-1995 (first entry)

DE Beta-peptide used to raise monoclonal antibody 59D8.

KM Inhibitor; thrombin; chimeric molecule; fibrin-binding; antibody;

KM hirudin; monoclonal; 59D8; fibrinopeptide B; coagulation; P79;

KM coronary stent implantation; adjunctive therapy; fibrinogen;

OS Synthetic.

PN W09425491-A.

PD 10-NOV-1994.

PF 03-MAY-1994; 94WO-US04881.

PR 03-MAY-1993; 93US-0058699.

PA (HARD) HARVARD COLLEGE.

PI (VDEM-) UNIV EMORY.

PI Bode C, Haber E, Runge M;

DR WPI; 1994-358195/44.

PT Fibrin-binding antibody linked to thrombin inhibitor - useful for

PT preventing blood coagulation by specifically targeting inhibitor

PS Example 1; Page 13; 53pp; English.

CC This sequence represents beta-peptide which was used to raise the

CC monoclonal antibody 59D8. The antibody binds fibrin and may be used

CC in the chimeric molecule of the invention. The chimeric molecule

CC further comprises a thrombin inhibitor linked to the fibrin-binding

CC antibody through a covalent linkage. The chimeric molecule allows

CC fibrin-specific antibody targeting of hirudin and other thrombin

CC inhibitors, which is more potent than thrombin on its own. The epitope

CC to which 59D8 binds becomes available only after thrombin cleaves

CC fibrinopeptide B. The chimeric protein may be used for preventing

CC coagulation of the blood. Anti-thrombin targeting can be esp. useful

CC in highly thrombogenic situations such as coronary stent implantation

CC and can be used as an adjunctive therapy with highly selective

CC thrombolytic agents. The thrombin inhibitor is localised to sites

CC of thrombin activity by the antibody which binds to thrombin but does

CC not cross react with uncleaved fibrinogen. The selectivity of

CC inhibition allows the total amount of thrombin inhibitor used to be

CC substantially reduced, resulting in a reduced potential for generalised

CC haemorrhaging.

SQ Sequence 7 AA;

Query Match 80.4%; Score 41; DB 15; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHRPLDK 7
1 GHRPLDK 7
DB 1 GHRPLDK 7

RESULT 9
AAR65792

ID AAR65792 standard; peptide; 7 AA.

AC AAR65792;
 XX PA
 DT 26-JUN-1995 (first entry)
 XX DE Fibrin-specific epitopic peptide.
 DE Fibrin-specific epitopic peptide; thrombi detection; fibrinogen;
 KW anti-fibrin-specific monoclonal antibodies.
 XX OS Synthetic.
 XX PN US5357042-A.
 XX PD 18-OCT-1994.
 XX PF 23-APR-1984; 84US-0603155.
 XX PR 23-APR-1984; 84US-0603155.
 PR 30-JAN-1986; 86US-0824228.
 PR 22-DEC-1989; 89US-0454954.
 PR 24-AUG-1992; 92US-0932729.
 XX PA (GENO) GEN HOSPITAL CORP.
 XX PI Haber E, Hui K, Matsueda GR;
 XX DR WPI; 1994-332411/41.
 XX PT Synthetic epitopic peptide(s) of variable length - capable of
 PT eliciting fibrin specific antibodies free of fibrinogen
 PT cross-reactivity.
 XX PS Claim 2; Column 18; 12pp; English.
 XX CC AAR65789-R65794 are synthetic peptides comprising fibrin-specific
 CC epitopic sequences, they can be used to prepare hybridoma cell
 CC lines, which produce anti-fibrin-specific monoclonal antibodies
 CC substantially devoid of fibrinogen cross-reactivity. These
 CC antibodies are useful in the in vivo and in vitro detection
 CC of thrombi and fibrin deposits.
 XX SQ Sequence 7 AA;
 Query Match 80.4%; Score 41; DB 15; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GHRPLDK 7
 DB 1 GHRPLDK 7
 RESULT 10
 AAR62686
 ID AAR62686 standard; peptide; 8 AA.
 XX AC AAR62686;
 XX DT 05-DEC-1990 (first entry)
 XX DE Human fibrin beta chain N-terminal.
 KM Fibrin; beta chain; N-terminal; monoclonal antibody; thrombosis.
 XX OS Synthetic.
 XX PN JPE3093800-A.
 XX PD 25-APR-1988.
 XX PF 08-OCT-1986; 86JP-0237876.
 PR 08-OCT-1986; 86JP-0237876.

XX XX
 XX PA (MITN) MITSUBISHI GAS CHEM KK.
 XX DR WPI; 1988-152086/22.
 XX PT New anti-human fibrin monoclonal antibody for diagnosing thrombosis
 PT - prepd. from hybridoma obtd. by applying cell fusion mouse spleen
 PT and mouse myeloma cells, and measures human fibrin.
 XX PS Claim 1; Page 1; 8pp; Japanese.
 XX CC The peptide is linked to a carrier protein via a linking agent and
 CC used to immunise mice. The mouse spleen cells and myeloma cell
 CC line can be fused to produce a hybridoma secreting MAb which bind
 CC specifically to human fibrin but not fibrinogen.
 XX SQ Sequence 8 AA;
 Query Match 80.4%; Score 41; DB 9; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 GHRPLDK 7
 DB 1 GHRPLDK 7
 RESULT 11
 AAR44837
 ID AAR44837 standard; peptide; 8 AA.
 XX AC AAR44837;
 XX DT 20-JUN-1994 (first entry)
 XX DE Human fibrin beta-chain N-terminal peptide A.
 XX KM Tissue plasminogen activator; t-PA; mutein; fibrin; antigen;
 KW anti-fibrin; monoclonal antibody; hybridoma; thrombolysis
 KW antithrombotic agent; bispecific antibody.
 XX OS Synthetic.
 XX PN JP05304992-A.
 XX PD 19-NOV-1993.
 XX PF 17-JUN-1992; 92JP-0158301.
 XX PR 20-JUN-1991; 91JP-0148936.
 XX PA (TAKE) TAKEDA CHEM IND LTD.
 XX DR WPI; 1993-408334/51.
 XX PT Hybrid monoclonal antibody - used for prepn. of thrombolytic drug
 PT having increased thrombolytic activity and specificity and
 PT reduced reactivity to fibrinogen
 XX PS Example 1; Page 14; 38pp; Japanese.
 XX CC Human fibrin beta-chain peptides A and B were synthesised and coupled
 CC to BSA for injection into mice. The peptides were used to raise
 CC antibodies to human fibrin. Monoclonal antibodies specific for fibrin
 CC are used in the production of bispecific monoclonal antibodies
 CC which also recognise truncated tPA muteins lacking the finger, EGF and
 CC Kringle 1 domains.
 XX SQ Sequence 8 AA;
 Query Match 80.4%; Score 41; DB 14; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 12

ID AAR63270 standard; peptide; 8 AA.

AC AAR63270;

DT 21-JUN-1995 (first entry)

DE Synthetic beta-peptide used to raise monoclonal antibody 59D8.

KW Inhibitor; thrombin; chimeric molecule; fibrin-binding; antibody;
KW hirudin; monoclonal; 59D8; fibrinopeptide B; coagulation; P79;
KW coronary stent implantation; adjunctive therapy; fibrinogen;
KW haemorrhage.

OS Synthetic.

PN W09425491-A.

PD 10-NOV-1994.

PF 03-MAY-1994; 94WO-US04881.

PR 03-MAY-1993; 93US-0058699.

PA (HARD) HARVARD COLLEGE.
(UYEM-) UNIV EMORY.

PI Bode C, Haber E, Runge M;

DR WPI; 1994-358195/44.

PT Fibrin-binding antibody linked to thrombin inhibitor - useful for
PT preventing blood coagulation by specifically targeting inhibitor
PT to site of thrombin activity

PS Example 1; Page 14; 53pp; English.

CC This sequence represents a synthetic beta-peptide which was used to
CC immunopurify the monoclonal antibody 59D8 which was raised against
CC beta-peptide (see also AAR63269). The antibody binds fibrin and may be
CC used in the chimeric molecule of the invention. The chimeric molecule
CC further comprises a thrombin inhibitor linked to the fibrin-binding
CC antibody through a covalent linkage. The chimeric molecule allows
CC fibrin-specific antibody targeting of hirudin and other thrombin
CC inhibitors, which is more potent than thrombin on its own. The epitope
CC to which 59D8 binds becomes available only after thrombin cleaves
CC fibrinopeptide B. The chimeric protein may be used for preventing
CC coagulation of the blood. Anti-thrombin targeting can be esp. useful
CC in highly thrombogenic situations such as coronary stent implantation
CC and can be used as an adjunctive therapy with highly selective
CC thrombolytic agents. The thrombin inhibitor is localised to sites
CC of thrombin activity by the antibody which binds to thrombin but does
CC not cross react with uncleaved fibrinogen. The selectivity of
CC inhibition allows the total amount of thrombin inhibitor used to be
CC substantially reduced, resulting in a reduced potential for generalised
CC haemorrhaging.

SQ Sequence 8 AA;

Query Match 80.4%; Score 41; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 13

ID AAR65793 standard; peptide; 8 AA.

AC AAR65793;

DT 26-JUN-1995 (first entry)

DE Fibrin-specific epitopic peptide.

KW Fibrin-specific epitopic peptides; thrombi detection; fibrinogen;
KW antifibrin-specific monoclonal antibodies.

OS Synthetic.

PH Key Location/Qualifiers

FT Misc-difference 8 /note= "May be absent and if present
FT may be bonded to keyhole limpet
FT hemocyanin."

PN US5357042-A.

PD 18-OCT-1994.

PF 23-APR-1984; 84US-0603155.

PR 23-APR-1984; 84US-0603155.

PR 30-JAN-1986; 86US-0824228.

PR 22-DEC-1989; 89US-0454954.

PR 24-AUG-1992; 92US-0932729.

PA (GERHO) GEN HOSPITAL CORP.

PI Haber E, Hui K, Matsueda GR;

DR WPI; 1994-332411/41.

PT Synthetic epitopic peptide(s) of variable length - capable of
PT eliciting fibrin specific antibodies free of fibrinogen
PT cross-reactivity.

PS Claim 3; Column 18; 12pp; English.

CC AAR65789-R65794 are synthetic peptides comprising fibrin-specific
CC epitopic sequences, they can be used to prepare hybridoma cell
CC lines, which produce antifibrin-specific monoclonal antibodies
CC substantially devoid of fibrinogen cross-reactivity. These
CC antibodies are useful in the in vivo and in vitro detection
CC of thrombi and fibrin deposits.

SQ Sequence 8 AA;

Query Match 80.4%; Score 41; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 14

ID AAR44838 standard; peptide; 12 AA.

AC AAR44838;

DT 20-JUN-1994 (first entry)

DE Human fibrin beta-chain peptide B.

XX Tissue plasminogen activator; t-PA; mitein; fibrin; antigen;
 KW anti-fibrin; monoclonal antibody; hybridoma; thrombolysis
 KM antithrombotic agent; bispecific antibody.
 XX
 OS Synthetic.
 XX
 PN JP05304992-A.
 XX
 PD 19-NOV-1993.
 XX
 PF 17-JUN-1992; 92JP-0158301.
 XX
 PR 20-JUN-1991; 91JP-0148936.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 DR WPI; 1993-408334/51.
 XX
 PT Hybrid monoclonal antibody - used for prepn. of thrombolytic drug
 PT having increased thrombolytic activity and specificity and
 PT reduced reactivity to fibrinogen
 XX
 PS Example 1; Page 14; 38pp; Japanese.
 XX
 CC Human fibrin beta-chain peptides A and B were synthesised and coupled
 CC to BSA for injection into mice. The peptides were used to raise
 CC antibodies to human fibrin. Monoclonal antibodies specific for fibrin
 CC are used in the production of bispecific monoclonal antibodies
 CC which also recognise truncated tPA mutants lacking the finger, EGF and
 CC Kringles 1 domains.
 XX
 SQ Sequence 12 AA;
 QY
 Query Match 80.4%; Score 41; DB 14; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.085;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 GHRPLDK 7
 6 GHRPLDK 12

RESULT 15
 AAB10666
 ID AAB10666 standard; peptide: 11 AA.
 XX
 AC AAB10666;
 XX
 DT 19-JAN-2001 (first entry)
 XX
 DE Fibrinogen-beta peptide fragment.
 XX
 KW Fibrinogen-alpha; polymer-encapsulated ingredient; drug release;
 KW bridging molecule.
 XX
 OS Unidentified.
 XX
 PN DE19905793-A1.
 XX
 PD 17-AUG-2000.
 XX
 PF 12-FEB-1999; 99DE-1005793.
 XX
 PR 12-FEB-1999; 99DE-1005793.
 XX
 PA (LAHA/) LAHANN J.
 PA (LEND/) LENDLEIN A.
 XX
 PI Lahann J, Lendlein A;
 XX
 DR WPI; 2000-566116/53.
 XX

PT Selective release of polymer-encapsulated ingredients, especially
 PT drugs, comprises crosslinking the polymer chains with cleavable
 PT bridging molecules -
 XX
 XX
 PS Disclosure; Page 3; 6pp; German.
 XX
 CC This invention describes a novel method for the selective release of
 CC polymer-encapsulated ingredients comprising incorporating reactive
 CC bridging molecules into the polymer during its manufacture, where the
 CC bridging molecules are cleavable by interaction with an endogenous
 CC reagent at the intended release site. The method is especially useful
 CC for drug release in vivo, preferably by incorporating amino acid,
 CC peptide, nucleic acid, polysaccharide, glycosaminoglycan, terpene or
 CC lipid bridging molecules into a water-swellable polymer (e.g. an acrylic
 CC polymer or polyvinylpyrrolidone), optionally protecting the bridging
 CC molecules against reaction with the cleaving reagent, by reaction with a
 CC carbonate, chloroformate, azidoformate or dicarbonate ester, thermally
 CC or photochemically activating the bridging molecules to crosslink the
 CC polymer chains, and introducing the crosslinked material into the body
 CC so that the bridging molecules will be cleaved by the reagent (e.g. an
 CC enzyme) at the intended release site, optionally after changing the pH
 CC to deprotect the bridging molecules or contacting the material with an
 CC enzyme that renders the bridging molecules cleavable by the cleaving
 CC reagent, especially a racemase, epimerase or exopeptidase. This sequence
 CC represents a fragment of fibrinogen-alpha which acts as a chemically
 CC active bridge which is used in the method of the invention.
 XX
 SQ Sequence 11 AA;
 QY
 Query Match 70.6%; Score 36; DB 21; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.84;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 GHRPLD 6
 6 GHRPLD 11

Search completed: June 27, 2003, 17:44:04
 Job time : 70 secs

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OM protein - protein search, using sw model

Run on: June 27, 2003, 17:46:03 ; Search time 48 Seconds
(without alignments)
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Title: US-10-019-439-2

Perfect score: 51

Sequence: 1 GHRPLDKR 9

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 424699 seqs, 109646833 residues

Total number of hits satisfying chosen parameters: 86429

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*
1: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubppaa/PCR_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70.6	10	9	US-10-142-935-9	Sequence 9, Appl1
2	70.6	15	9	US-10-142-935-8	Sequence 8, Appl1
3	70.6	15	9	US-10-068-569-5	Sequence 5, Appl1
4	52.9	12	9	US-09-954-385-130	Sequence 130, App
5	51.0	13	9	US-09-892-877-278	Sequence 278, App
6	51.0	15	9	US-09-948-783-290	Sequence 290, App
7	51.0	17	9	US-09-983-802-349	Sequence 349, App
8	51.0	18	9	US-10-083-357-1073	Sequence 1073, App
9	51.0	19	9	US-09-892-877-383	Sequence 383, App
10	51.0	19	9	US-09-948-783-383	Sequence 383, App
11	51.0	19	9	US-10-225-567A-2064	Sequence 2064, App
12	49.0	9	9	US-09-881-572A-3	Sequence 3, Appl1
13	49.0	9	9	US-10-040-862-9737	Sequence 9737, App
14	49.0	9	9	US-10-040-862-10000	Sequence 10000, App
15	49.0	9	9	US-10-040-862-10018	Sequence 10018, App
16	49.0	9	9	US-10-040-862-10187	Sequence 10187, App
17	49.0	9	9	US-10-040-862-10233	Sequence 10233, App
18	49.0	14	9	US-09-880-748-2409	Sequence 2409, App
19	47.1	7	10	US-09-947-137-27	Sequence 27, Appl1

20	24	47.1	9	US-09-968-561A-54	Sequence 54, Appl1
21	24	47.1	9	US-09-782-672-49	Sequence 49, Appl1
22	24	47.1	9	US-09-192-854-36	Sequence 36, Appl1
23	24	47.1	9	US-09-984-056-56	Sequence 56, Appl1
24	24	47.1	9	US-09-984-057-56	Sequence 57, Appl1
25	24	47.1	12	US-10-185-815-20	Sequence 20, Appl1
26	24	47.1	14	US-09-880-748-2369	Sequence 2369, App
27	24	47.1	14	US-09-880-748-2444	Sequence 2444, App
28	24	47.1	14	US-09-880-748-2480	Sequence 2480, App
29	24	47.1	14	US-09-880-748-2513	Sequence 2513, App
30	24	47.1	14	US-09-880-748-2538	Sequence 2538, App
31	24	47.1	16	US-10-100-861-4	Sequence 4, Appl1
32	24	47.1	16	US-09-880-748-2853	Sequence 2853, App
33	24	47.1	18	US-08-424-5508-593	Sequence 593, App
34	24	47.1	19	US-10-211-088-250	Sequence 250, App
35	23	45.1	7	US-09-821-687-7	Sequence 7, Appl1
36	23	45.1	11	US-09-876-904A-478	Sequence 478, App
37	23	45.1	12	US-09-876-904A-247	Sequence 247, App
38	23	45.1	17	US-10-225-567A-920	Sequence 920, App
39	23	45.1	17	US-09-821-687-5	Sequence 5, Appl1
40	23	45.1	18	US-10-223-711-2	Sequence 12, Appl1
41	22	43.1	8	US-10-318-780-12	Sequence 12, Appl1
42	22	43.1	9	US-10-087-065-642	Sequence 642, App
43	22	43.1	9	US-09-935-682-29	Sequence 29, Appl1
44	22	43.1	9	US-09-954-166-15	Sequence 15, Appl1
45	22	43.1	10	US-09-947-137-21	Sequence 21, Appl1

ALIGNMENTS

RESULT 1
US-10-142-935-9
Sequence 9, Application US/10142935
Publication No. US20030044418A1
GENERAL INFORMATION:
APPLICANT: DAVIS, Stacey
TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULAT
FILE REFERENCE: P07201US01/BAS
CURRENT FILING DATE: 2002-05-13
PRIORITY FILING DATE: 2001-05-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 10
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-10-142-935-9

Query Match 70.6%; Score 36; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
DB 5 GHRPLD 10

RESULT 2
US-10-142-935-8
Sequence 8, Application US/10142935
Publication No. US20030044418A1
GENERAL INFORMATION:
APPLICANT: DAVIS, Stacey
TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR INHIBITING THROMBIN-INDUCED COAGULAT
FILE REFERENCE: P07201US01/BAS
CURRENT FILING DATE: 2002-05-13
PRIORITY FILING DATE: 2002-05-13
CURRENT APPLICATION NUMBER: US 60/290,072
PRIOR APPLICATION NUMBER: US 60/290,072

PRIOR FILING DATE: 2001-05-13
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 15
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-10-142-935-8

Query Match
Best Local Similarity 70.6%; Score 36; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPLD 6
Db 10 GHRPLD 15

RESULT 3
US-10-068-569-5
Sequence 5, Application US/10068569
Patent No. US20020160975A1
GENERAL INFORMATION:
APPLICANT: Srinivasula, Srinivasa M.
APPLICANT: Fernandes-Alnemri, Teresa
APPLICANT: Alnemri, Emad S.
TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
FILE REFERENCE: 480140.475
CURRENT APPLICATION NUMBER: US/10/068,569
CURRENT FILING DATE: 2002-02-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 15
TYPE: PRT
ORGANISM: Mus musculus
US-10-068-569-5

Query Match
Best Local Similarity 52.9%; Score 27; DB 9; Length 15;
Best Local Similarity 71.4%; Pred. No. 63;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHRPLD 7
Db 7 GHRPLDQ 13

RESULT 4
US-09-954-385-130
Sequence 130, Application US/09954385
Publication No. US20030100467A1
GENERAL INFORMATION:
APPLICANT: Aehle, Wolfgang
APPLICANT: Baldwin, Toby L.
APPLICANT: Van Gasteel, Francis J.C.
APPLICANT: Janssen, Gisselle G.
APPLICANT: Murray, Christopher J.
APPLICANT: Wang, Huang
APPLICANT: Winetzk, Deborah S.
TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
FILE REFERENCE: GC690
CURRENT APPLICATION NUMBER: US/09/954,385
CURRENT FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 433
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 130
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: binding peptide

US-09-954-385-130

Query Match
Best Local Similarity 51.0%; Score 26; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRP 4
Db 1 GHRP 4

RESULT 5
US-09-892-877-278
Sequence 278, Application US/09892877
Publication No. US20030077809A1
GENERAL INFORMATION:
APPLICANT: Ruben et. al.
TITLE OF INVENTION: 97 Human secreted proteins
FILE REFERENCE: P2028P1
CURRENT APPLICATION NUMBER: US/09/892,877
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/437,658
PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-10
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 278
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
US-09-892-877-278

Query Match
Best Local Similarity 51.0%; Score 26; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRP 4
Db 9 GHRP 12

RESULT 6
US-09-948-783-290
Sequence 290, Application US/09948783
Publication No. US20030100051A1
GENERAL INFORMATION:
APPLICANT: Ruben et. al.
TITLE OF INVENTION: 97 Human secreted proteins
FILE REFERENCE: P2028P2
CURRENT APPLICATION NUMBER: US/09/948,783
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/231,846
PRIOR FILING DATE: 2000-09-11
PRIOR APPLICATION NUMBER: 09/892,877
PRIOR FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: 09/437,658
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: PCT/US99/09847
PRIOR FILING DATE: 1999-05-06
PRIOR APPLICATION NUMBER: 60/085,093
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/085,094
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/085,105
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/085,180
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/085,927
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,906
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,924
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: 60/085,922

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? PRIOR FILING DATE: 1998-05-18
? PRIOR APPLICATION NUMBER: 60/085,921
? PRIOR FILING DATE: 1998-05-18
? PRIOR APPLICATION NUMBER: 60/085,923
? PRIOR FILING DATE: 1998-05-18
? PRIOR APPLICATION NUMBER: 60/085,925
? PRIOR FILING DATE: 1998-05-18
? PRIOR APPLICATION NUMBER: 60/085,928
? PRIOR FILING DATE: 1998-05-18
? PRIOR APPLICATION NUMBER: 60/085,920
? PRIOR FILING DATE: 1998-05-18
? NUMBER OF SEQ ID NOS: 465
? SOFTWARE: PatentIn Ver. 2.0
  SEQ ID NO 290
    LENGTH: 15
    TYPE: prt
? ORGANISM: Homo sapiens
? US-09-948-783-290

```

Query Match	51.0%	Score	26	DB	9	Length	15
Best Local Similarity	100.0%	Pred. No.	99				
Matches	4	Conservative	0	Mismatches	0	Indels	0
						Gaps	0

Qy	1	GHRP	4
Db	9	GHRP	12

RESULT 7
US-09-983-802-349

```

; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION:

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; CURRENT APPLICATION NUMBER: US/09/983,802
 ; CURRENT FILING DATE: 2001-10-25

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/13684
 PRIOR FILING DATE: 1998-07-07

PRIOR APPLICATION NUMBER: 60/052,793
PRIOR FILING DATE: 1997-07-08

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PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
 PRIOR APPLICATION NUMBER: 60/052,732
 PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
 PRIOR APPLICATION NUMBER: 60/052,732

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: 60/051,932

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: 60/051, 930

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: 60/051,920
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: 60/051,920

PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: 60/052,795
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: 60/052,795

; PRIOR FILING DATE: 1997-07-08
 ; PRIOR APPLICATION NUMBER: 60/051,928

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1 PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
2 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,722
3 PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
4 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,723
5 PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
6 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,948
7 PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
8 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,949
9 PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
10 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,953
11 PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
12 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,950
13 PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
14 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,947
15 PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
16 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,964
17 PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
18 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/056,360
19 PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
20 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,684
21 PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
22 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,984
23 PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
24 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,954
25 PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
26 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,785
27 PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
28 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,664
29 PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
30 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,660
31 PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
32 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,661
33 NUMBER OF SEQ ID NOS: 672
34 SOFTWARE: PatentIn Ver. 2.0
35 SEQ ID NO 349
36 LENGTH: 17
37 TYPE: PRT
38 ORGANISM: Homo sapiens
39 JS-09-983-802-349

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Query March	51.0%	Score 26;	DB 9;	length 17;
Best Local Similarity	83.3%	Pred. No. 1.1e+02;		
Matches	5;	Conservative	1;	Indels 0;
		Mismatches	1;	Gaps 0;

Db 1 PUDKAR 6

RESULT 8
US-10-083-357-1073

GENERAL INFORMATION:
FACULTATION NO.: 0020050057570814
APPLICANT: Qiangdong Zeng et al.

FILE REFERENCE: 02/30-030
CURRENT APPLICATION NUMBER: US/10/083,357
CURRENT FILING DATE: 2002-02-27

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; SEQ ID NO 10/3
;
; LENGTH: 18
;
; TYPE: PRT

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Query Match	51.0%	Score 26:	DB 9:	length 18:
US-10-083-357-10/3				

Matches	4;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
1	CHRP	4							

Db 13 GHRP 16

RESULT 9

US-09-892-877-383

Sequence 383, Application US/09892877

Publication No. US20030077809A1

GENERAL INFORMATION:

APPLICANT: Ruben et. al.

TITLE OF INVENTION: 97 Human secreted proteins

FILE REFERENCE: P2028P1

CURRENT APPLICATION NUMBER: US/09/892,877

CURRENT FILING DATE: 2001-06-28

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/437,658

PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-10

NUMBER OF SEQ ID NOS: 461

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 383

LENGTH: 19

TYPE: PRT

ORGANISM: Homo sapiens

US-09-892-877-383

Query Match

Best Local Similarity 51.0%; Score 26; DB 9; Length 19;

Best Local Similarity 50.0%; Pred. No. 1.3e+02;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 HRPDKR 9

Db 7 HKPTTKR 14

RESULT 10

US-09-948-783-383

Sequence 383, Application US/09948783

Publication No. US20030100051A1

GENERAL INFORMATION:

APPLICANT: Ruben et. al.

TITLE OF INVENTION: 97 Human secreted proteins

FILE REFERENCE: P2028P2

CURRENT APPLICATION NUMBER: US/09/948,783

CURRENT FILING DATE: 2001-09-10

PRIOR APPLICATION NUMBER: 60/231,846

PRIOR FILING DATE: 2000-09-11

PRIOR APPLICATION NUMBER: 09/892,877

PRIOR FILING DATE: 2001-06-28

PRIOR APPLICATION NUMBER: 09/437,658

PRIOR FILING DATE: 1999-11-10

PRIOR APPLICATION NUMBER: PCT/US99/09847

PRIOR FILING DATE: 1999-05-06

PRIOR APPLICATION NUMBER: 60/085,093

PRIOR FILING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: 60/085,094

PRIOR FILING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: 60/085,105

PRIOR FILING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: 60/085,180

PRIOR FILING DATE: 1998-05-12

PRIOR APPLICATION NUMBER: 60/085,927

PRIOR FILING DATE: 1998-05-18

PRIOR APPLICATION NUMBER: 60/085,906

PRIOR FILING DATE: 1998-05-18

PRIOR APPLICATION NUMBER: 60/085,924

PRIOR FILING DATE: 1998-05-18

PRIOR APPLICATION NUMBER: 60/085,922

PRIOR FILING DATE: 1998-05-18

PRIOR APPLICATION NUMBER: 60/085,921

PRIOR FILING DATE: 1998-05-18

PRIOR APPLICATION NUMBER: 60/085,923

PRIOR FILING DATE: 1998-05-18

PRIOR APPLICATION NUMBER: 60/085,925

PRIOR FILING DATE: 1998-05-18

PRIOR APPLICATION NUMBER: 60/085,928

PRIOR FILING DATE: 1998-05-18

PRIOR APPLICATION NUMBER: 60/085,920

PRIOR FILING DATE: 1998-05-18

NUMBER OF SEQ ID NOS: 465

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 383

LENGTH: 19

TYPE: PRT

ORGANISM: Homo sapiens

US-09-948-783-383

Query Match

Best Local Similarity 51.0%; Score 26; DB 9; Length 19;

Best Local Similarity 50.0%; Pred. No. 1.3e+02;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 HRPDKR 9

Db 7 HKPTTKR 14

RESULT 11

US-10-225-567A-2064

Sequence 2064, Application US/10225567A

Publication No. US20030113798A1

GENERAL INFORMATION:

APPLICANT: Lifespan Biosciences

APPLICANT: Brown, Joseph P.

APPLICANT: Burner, Glenna C.

APPLICANT: Roush, Christine L.

TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR

FILE REFERENCE: 1920-4-4

CURRENT APPLICATION NUMBER: US/10/225,567A

CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/257,144

PRIOR FILING DATE: 2000-12-19

NUMBER OF SEQ ID NOS: 2292

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2064

LENGTH: 19

TYPE: PRT

ORGANISM: Homo sapiens

US-10-225-567A-2064

Query Match

Best Local Similarity 51.0%; Score 26; DB 9; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRP 4

Db 8 GHRP 11

RESULT 12

US-09-881-572A-3

Sequence 3, Application US/09881572A

Patent No. US20020164583A1

GENERAL INFORMATION:

APPLICANT: Roth, Monica;

APPLICANT: Bupp, Keith;

TITLE OF INVENTION: University of Medicine and Dentistry of New Jersey

FILE REFERENCE: 601-1-095

CURRENT APPLICATION NUMBER: US/09/881,572A

CURRENT FILING DATE: 2002-03-05

PRIOR APPLICATION NUMBER: 60/212,239

PRIOR FILING DATE: 2000-06-16

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn version 3.0

SEQ ID NO 3

LENGTH: 9

TYPE: PRT

ORGANISM: moloney murine leukemia virus

US-09-881-572A-3

Query Match 49.0%; Score 25; DB 9; Length 9;
Best Local Similarity 57.1%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 HRPDKK 8
Db 2 HRPDKK 8

RESULT 13

US-10-040-862-9737
; Sequence 9737, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9737
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-9737

Query Match 49.0%; Score 25; DB 9; Length 9;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GHRPLDKK 8
Db 2 GHVPIQSK 9

RESULT 14

US-10-040-862-10000
; Sequence 10000, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therap
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10000
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-10000

Query Match 49.0%; Score 25; DB 9; Length 9;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GHRPLDKK 8
Db 1 GHVPIQSK 8

RESULT 15

US-10-040-862-10018
; Sequence 10018, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therap
; FILE REFERENCE: 014058-013520US
; CURRENT APPLICATION NUMBER: US/10/040,862
; CURRENT FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545

; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/223,378
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 09/796,692
; PRIOR FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 10467
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10018
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-040-862-10018

Query Match 49.0%; Score 25; DB 9; Length 9;
Best Local Similarity 50.0%; Pred. No. 3.8e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 GHRPLDKK 8
| | | | |
| | | | |
Db 1 GHVPIQSK 8

Search completed: June 27, 2003, 17:55:14
Job time : 49 secs

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OM protein - protein search, using sw model

Run on: June 27, 2003, 17:42:53 ; Search time 25 seconds
(without alignments)
10.592 Million cell updates/sec

Title: US-10-019-439-2

Perfect score: 51

Sequence: 1 GHRPLDKKR 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 127244

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep: *
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep: *
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep: *
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	10	2	US-08-448-547-1
2	41	80.4	7	1	US-08-058-699-10
3	41	80.4	8	1	US-08-058-699-11
4	27	52.9	18	2	US-07-876-941A-30
5	26	51.0	4	2	US-08-747-137-79
6	26	51.0	10	2	US-08-556-597-84
7	26	51.0	11	3	US-08-592-500-41
8	26	51.0	11	3	US-08-195-006-41
9	26	51.0	11	5	PCT-US94-07644A-41
10	26	51.0	13	1	US-08-480-463-10
11	26	51.0	13	3	US-08-990-015-9
12	26	51.0	13	3	US-08-469-433B-10
13	26	51.0	13	5	PCT-US94-07916-10
14	26	51.0	17	4	US-09-227-357-349
15	26	51.0	19	4	US-08-827-962-2
16	25	49.0	9	4	US-09-258-754-234
17	25	49.0	9	4	US-09-042-107-234
18	25	49.0	11	1	US-08-547-182-11
19	24	47.1	7	4	US-09-084-605B-27
20	24	47.1	7	6	5180668-2
21	24	47.1	7	6	5180668-4
22	24	47.1	8	6	5180668-7
23	24	47.1	10	2	US-08-556-597-122
24	24	47.1	12	4	US-09-478-479-8
25	24	47.1	12	4	US-09-479-479-9
26	24	47.1	12	4	US-09-297-851-8
27	24	47.1	12	4	US-09-297-851-9

28	24	47.1	13	6	5395760-16	Patent No. 5395760
29	24	47.1	14	1	US-08-141-324-8	Sequence 8, Appli
30	24	47.1	14	1	US-08-541-502-8	Sequence 8, Appli
31	24	47.1	14	2	US-08-796-598-17	Sequence 17, Appl
32	24	47.1	14	2	US-08-447-175A-17	Sequence 17, Appl
33	24	47.1	15	4	US-08-602-999A-306	Sequence 306, App
34	24	47.1	15	4	US-09-500-124-306	Sequence 306, App
35	24	47.1	18	4	US-08-469-260A-593	Sequence 593, App
36	24	47.1	19	4	US-09-025-596-39	Sequence 39, Appl
37	23	45.1	7	1	US-08-240-514-9	Sequence 9, Appli
38	23	45.1	7	2	US-08-612-302A-9	Sequence 9, Appli
39	23	45.1	9	3	US-08-159-339A-417	Sequence 417, App
40	23	45.1	10	1	US-08-173-508-10	Sequence 10, Appl
41	23	45.1	10	1	US-07-965-667A-3	Sequence 3, Appli
42	23	45.1	10	2	US-08-265-310-10	Sequence 10, Appl
43	23	45.1	10	3	US-08-484-819-3	Sequence 3, Appli
44	23	45.1	10	5	PCT-US93-10197-3	Sequence 3, Appli
45	23	45.1	13	5	PCT-US93-08386-32	Sequence 32, Appli

ALIGNMENTS

RESULT 1
US-08-448-547-1
Sequence 1, Application US/08448547
Patent No. 5821068
GENERAL INFORMATION:
APPLICANT: Soe, Gilbu
APPLICANT: Kohno, Isao
APPLICANT: Imuzuka, Kimiko
APPLICANT: Ito, Yumiko
TITLE OF INVENTION: ANTI-HUMAN SOLUBLE FIBRIN ANTIBODY,
HYBRIDOMA, AND IMMUNOSSAYING METHOD
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPHEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/448,547
FILING DATE: 30-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/01844
FILING DATE: 01-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-297325
FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: O-38931
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-448-547-1

Query Match 100.0%; Score 51; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00062;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDKR 9
Db 1 GHRPLDKR 9

RESULT 2

US-08-058-699-10
Sequence 10, Application US/08058699
Patent No. 5443827
GENERAL INFORMATION:
APPLICANT: Edgar Haber
APPLICANT: Christoph Bode
TITLE OF INVENTION: FIBRIN-TARGETED INHIBITORS OF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/058,699
FILING DATE: 19930503
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: N/A
FILING DATE: N/A
ATTORNEY/AGENT INFORMATION:
NAME: Janis K. Fraser, Ph.D.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 7
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: Linear
US-08-058-699-10

Query Match 80.4%; Score 41; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 3

US-08-058-699-11
Sequence 11, Application US/08058699
Patent No. 5443827
GENERAL INFORMATION:
APPLICANT: Edgar Haber
APPLICANT: Christoph Bode
APPLICANT: Marshall S. Runge
TITLE OF INVENTION: FIBRIN-TARGETED INHIBITORS OF

TITLE OF INVENTION: THROMBIN
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/058,699
FILING DATE: 19930503
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: N/A
FILING DATE: N/A
ATTORNEY/AGENT INFORMATION:
NAME: Janis K. Fraser, Ph.D.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05433/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: Linear
US-08-058-699-11

Query Match 80.4%; Score 41; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHRPLDK 7
Db 1 GHRPLDK 7

RESULT 4

US-07-876-941A-30
Sequence 30, Application US/07876941A
Patent No. 5885768
GENERAL INFORMATION:
APPLICANT: Reyes, Gregory R.
APPLICANT: Bradley, Daniel W.
APPLICANT: Tam, Albert W.
APPLICANT: Mitchell, Carl
TITLE OF INVENTION: Hepatitis E Virus Peptide Antigen and
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,941A
FILING DATE: 01-MAY-1992

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 822,335
FILING DATE: 17-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 505,888
FILING DATE: 05-APRIL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 420,921
FILING DATE: 13-OCTOBER-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 367,486
FILING DATE: 16-JUNE-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 336,672
FILING DATE: 11-APRIL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 208,997
FILING DATE: 17-JUNE-1988
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0093.33
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: Fig. 11, ORF 1, aa 1237-1254
US-07-876-941A-30

Query Match 52.9%; Score 27; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 49;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRPL 5
|||:
Db 14 GHRPV 18

RESULT 5
US-08-747-137-79
Sequence 79, Application US/08747137
Patent No. 594503
GENERAL INFORMATION:
APPLICANT: YEN, Richard C.K.
TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
OPERATING SYSTEM: THERAPEUTIC AND DIAGNOSTIC USE
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,137
FILING DATE: 12-NOV-1996
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,546
FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,831
FILING DATE: 01-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/959,560
FILING DATE: 13-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/641,720
FILING DATE: 15-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 016197-000840US
TELEPHONE: 415-576-0200
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
US-08-747-137-79

Query Match 51.0%; Score 26; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1,9e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRP 4
|||:
Db 1 GHRP 4

RESULT 6
US-08-556-597-84
Sequence 84, Application US/08556597
Patent No. 5877155
GENERAL INFORMATION:
APPLICANT: Miller, Jonathan L.
TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
OPERATING SYSTEM: HUMAN PLATELET GLYCOPROTEIN Ib/IX
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,597
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,330
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Timlan, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-556-597-84

Query Match 51.0%; Score 26; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 HRPIDKX 8
Db 1 HRPISMK 7

RESULT 7
US-08-592-500-41
Sequence 41, Application US/08592500
Patent No. 6005089
GENERAL INFORMATION:
APPLICANT: Lanza, Francois
APPLICANT: Phillips, David R.
APPLICANT: Cazenave, Jean-Pierre
TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Knourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,500
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,455
FILING DATE: 09-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 12418-28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..11
OTHER INFORMATION: /note= "Amino acid sequence of the
OTHER INFORMATION: human fibrinogen (Fg) B-beta chain thrombin
OTHER INFORMATION: cleavage site."
FEATURE:
NAME/KEY: Region
LOCATION: 7..8
OTHER INFORMATION: /note= "Amino acid residues
OTHER INFORMATION: identical to GPV."
FEATURE:
NAME/KEY: Region
LOCATION: 11

OTHER INFORMATION: /note= "Amino acid residue
OTHER INFORMATION: identical to GPV."
US-08-592-500-41

Query Match 51.0%; Score 26; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GHRP 4
Db 8 GHRP 11

RESULT 8
US-08-195-006-41
Sequence 41, Application US/08195006
Patent No. 6083688
GENERAL INFORMATION:
APPLICANT: Lanza, Francois
APPLICANT: Phillips, David R.
APPLICANT: Cazenave, Jean-Pierre
TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Knourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,006
FILING DATE: 10-FEB-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,455
FILING DATE: 09-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 12418-28
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..11
OTHER INFORMATION: /note= "Amino acid sequence of the
OTHER INFORMATION: human fibrinogen (Fg) B-beta chain thrombin
OTHER INFORMATION: cleavage site."
FEATURE:
NAME/KEY: Region
LOCATION: 7..8
OTHER INFORMATION: /note= "Amino acid residues
OTHER INFORMATION: identical to GPV."
FEATURE:
NAME/KEY: Region
LOCATION: 11
OTHER INFORMATION: /note= "Amino acid residue
OTHER INFORMATION: identical to GPV."
US-08-195-006-41

Query Match 51.0%; Score 26; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRP 4
|||
Db 8 GHRP 11

RESULT 9

PCT-US94-07644A-41
; Sequence 41, Application PC/TUS9407644A
; GENERAL INFORMATION:
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: Platelet Glycoprotein V Gene and Uses
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07644A
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 012418-003000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..11
; OTHER INFORMATION: /note= "Amino acid sequence of the
; OTHER INFORMATION: human fibrinogen (Fg) B-beta chain thrombin
; OTHER INFORMATION: cleavage site."
; FEATURE:
; NAME/KEY: Region
; LOCATION: 7..8
; OTHER INFORMATION: /note= "Amino acid residues
; OTHER INFORMATION: identical to GPV."
; FEATURE:
; NAME/KEY: Region
; LOCATION: 11
; OTHER INFORMATION: /note= "Amino acid residue
; OTHER INFORMATION: identical to GPV."
PCT-US94-07644A-41

Query Match 51.0%; Score 26; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHRP 4
|||
Db 8 GHRP 11

RESULT 10
US-08-480-463-10
; Sequence 10, Application US/08480463
; Patent No. 5661025
; GENERAL INFORMATION:
; APPLICANT: SZOKA, FRANCIS C.
; APPLICANT: HENSLEY, JEAN
; TITLE OF INVENTION: SELF-ASSEMBLING POLYNUCLEOTIDE
; TITLE OF INVENTION: DELIVERY SYSTEM COMPRISING DENDRIMER
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: CROSBY HEAPEY ROACH & MAY
; STREET: 1999 HARRISON ST
; CITY: OAKLAND
; STATE: CA
; COUNTRY: USA
; ZIP: 94612

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1/ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,463
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/092,200
; FILING DATE: 14-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KOENIG, NATHAN P.
; REGISTRATION NUMBER: 38,210
; REFERENCE/DOCKET NUMBER: 13054.00110
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 763-2000
; TELEFAX: (510) 273-8832
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-480-463-10

Query Match 51.0%; Score 26; DB 1; Length 13;
Best Local Similarity 44.4%; Pred. No. 55;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDKR 9
|:|:|:|:
Db 2 GYGPDKRK 10

RESULT 11

US-08-990-015-9
; Sequence 9, Application US/08990015A
; Patent No. 6093701
; GENERAL INFORMATION:
; APPLICANT: Budker, Vladimir
; APPLICANT: Hagstrom, James E.
; APPLICANT: Sebestyen, Magdolna G.
; APPLICANT: Wolff, Jon A.
; TITLE OF INVENTION: A METHOD FOR COVALENT ATTACHMENT OF COMPOUNDS TO GENES
; FILE REFERENCE: Covalent Attachment to Genes
; CURRENT APPLICATION NUMBER: US/08/990,015A
; EARLIER FILING DATE: 1997-12-12
; EARLIER APPLICATION NUMBER: 60/050842
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9

LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:SV40 NLS (mNLS)
US-08-990-015-9

Query Match 51.0%; Score 26; DB 3; Length 13;
Best Local Similarity 44.4%; Pred. No. 55;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDKR 9
Db 2 GYGPKDKRK 10

RESULT 12
US-08-469-433B-10
Sequence 10, Application US/08469433B
Patent No. 613946
GENERAL INFORMATION:
APPLICANT: SZOKA, FRANCIS C.
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: SELF-ASSEMBLING POLYNUCLEOTIDE
TITLE OF INVENTION: DELIVERY SYSTEM COMPRISING DENDRIMER
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: CROSBY HEAPEY ROACH & MAY
STREET: 1999 HARRISON ST
CITY: OAKLAND
STATE: CA
COUNTRY: USA
ZIP: 94612
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.11
SOFTWARE: Wordperfect 6.1/ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,433B
FILING DATE: 06-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KOENIG, NATHAN P.
REGISTRATION NUMBER: 38,210
REFERENCE/DOCKET NUMBER: 13054.11100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 763-2000
TELEFAX: (510) 273-8832
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-469-433B-10

Query Match 51.0%; Score 26; DB 3; Length 13;
Best Local Similarity 44.4%; Pred. No. 55;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDKR 9
Db 2 GYGPKDKRK 10

RESULT 13
PCT-US94-07916-10
Sequence 10, Application PC/TUS9407916
GENERAL INFORMATION:
APPLICANT: SZOKA, FRANCIS C.

APPLICANT: HENSLEY, JEAN
TITLE OF INVENTION: SELF-ASSEMBLING POLYNUCLEOTIDE
TITLE OF INVENTION: DELIVERY SYSTEM COMPRISING DENDRIMER
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBBINS, BERLINER & CARSON
STREET: 201 NORTH FIGUEROA STREET
CITY: LOS ANGELES
STATE: CA
COUNTRY: USA
ZIP: 90012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 5.1 / ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07916
FILING DATE: 14-JUL-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: BERLINER, ROBERT
REGISTRATION NUMBER: 20,121
REFERENCE/DOCKET NUMBER: 5555-242
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 977-1001
TELEFAX: (213) 977-1003
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US94-07916-10

Query Match 51.0%; Score 26; DB 5; Length 13;
Best Local Similarity 44.4%; Pred. No. 55;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 GHRPLDKR 9
Db 2 GYGPKDKRK 10

RESULT 14
US-09-227-357-349
Sequence 349, Application US/09227357
Patent No. 6342581
GENERAL INFORMATION:
APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: P2010P1
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,925
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,929
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,803
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,931
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,932

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; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,916
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,930
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,918
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,920
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,733
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/052,795
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,919
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/051,928
; EARLIER FILING DATE: 1997-07-08
; EARLIER APPLICATION NUMBER: 60/055,722
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,723
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,948
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,949
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,953
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,950
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,947
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,964
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/056,360
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,684
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,984
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/055,954
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/058,785
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,664
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,660
; EARLIER FILING DATE: 1997-09-12
; EARLIER APPLICATION NUMBER: 60/058,661
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 349
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-227-357-349

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Query Match          51.0%; Score 26; DB 4; Length 17;
Best Local Similarity 83.3%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      4 PLDKKR 9
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Db      1 PLDKKR 6

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RESULT 15
US-08-827-962-2
; Sequence 2, Application US/08827962A
; Patent No. 6258944
; GENERAL INFORMATION:
; APPLICANT: MERCK & CO., INC.
; TITLE OF INVENTION: OB RECEPTOR ISOFORMS AND NUCLEIC ACIDS

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; TITLE OF INVENTION: ENCODING THEM
; FILE REFERENCE: 19693
; CURRENT APPLICATION NUMBER: US/08/827,962A
; CURRENT FILING DATE: 1997-05-06
; PRIOR APPLICATION NUMBER: 60/016,899
; PRIOR FILING DATE: 1996-05-06
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Rattus No. 6258944vegicus
US-08-827-962-2

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Query Match          51.0%; Score 26; DB 4; Length 19;
Best Local Similarity 55.6%; Pred. No. 81;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY      1 GHRPLDKKR 9
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Db      10 GHKDLISKR 18

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Search completed: June 27, 2003, 17:47:17
Job time : 27 secs

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